

FIG. 1A

```

1  agggagagggc agtgaccatg aaggctgtgc tgcttgccct gttgatggca
51  ggcttgggccc tgcagccagg cactgccctg ctgtgctact cctgcaaagc
101 ccaggtgagc aacgaggact gcctgcaggt ggagaactgc acccagctgg
151 gggagcagtg ctggaccgcg cgcacccgcg cagttggcct cctgaccgtc
201 atcagcaaag gctgcagctt gaactgcgtg gatgactcac aggactacta
251 cgtgggcaag aagaacatca cgtgctgtga caccgacttg tgcaacgcca
301 gcggggccca tgccctgcag ccggctgccg ccatccttgc gctgctccct
351 gcactcggcc tgctgctctg gggacccggc cagctatagg ctctgggggg
401 ccccgctgca gccacactg ggtgtggtgc cccaggcctt tgtgccactc
451 ctcacagaac ctggcccagt gggagcctgt cctggttcct gaggcacatc
501 ctaacgcaag tttgaccatg tatgtttgca ccccttttcc ccnaaccctg
551 accttcccat gggccttttc caggattccn accnggcaga tcagttttag
601 tganacanat ccgcntgcag atggcccctc caaccntttt tgttgntggt
651 tccatggccc agcatttttc acccttaacc ctgtgttcag gcacttnttc
701 cccaggaag ccttccctgc ccacccatt tatgaattga gccaggtttg
751 gtccgtggtg tccccgcac ccagcagggg acaggcaatc aggagggccc
801 agtaaaggct gagatgaagt ggactgagta gaactggagg acaagagttg
851 acgtgagttc ctgggagttt ccagagatgg ggcctggagg cctggaggaa
901 ggggccaggc ctcacatttg tgggntccc gaatggcagc ctgagcacag
951 cgtaggccct taataaacac ctgttgata agccaaaaaa aaaaaaaa

```

FIG. 1B

```

MKAVLLALLMAGLALQPGTALLCYSCKAQVSNECLQV
ENCTQLGEQCWTARIRAVGLLTVISKGCSLNCVDDS
QDYYVGKKNITCCDTDLNCSGAHALQPAAAILALLPAL
GLLLWGPGQL

```

# FIG. 2

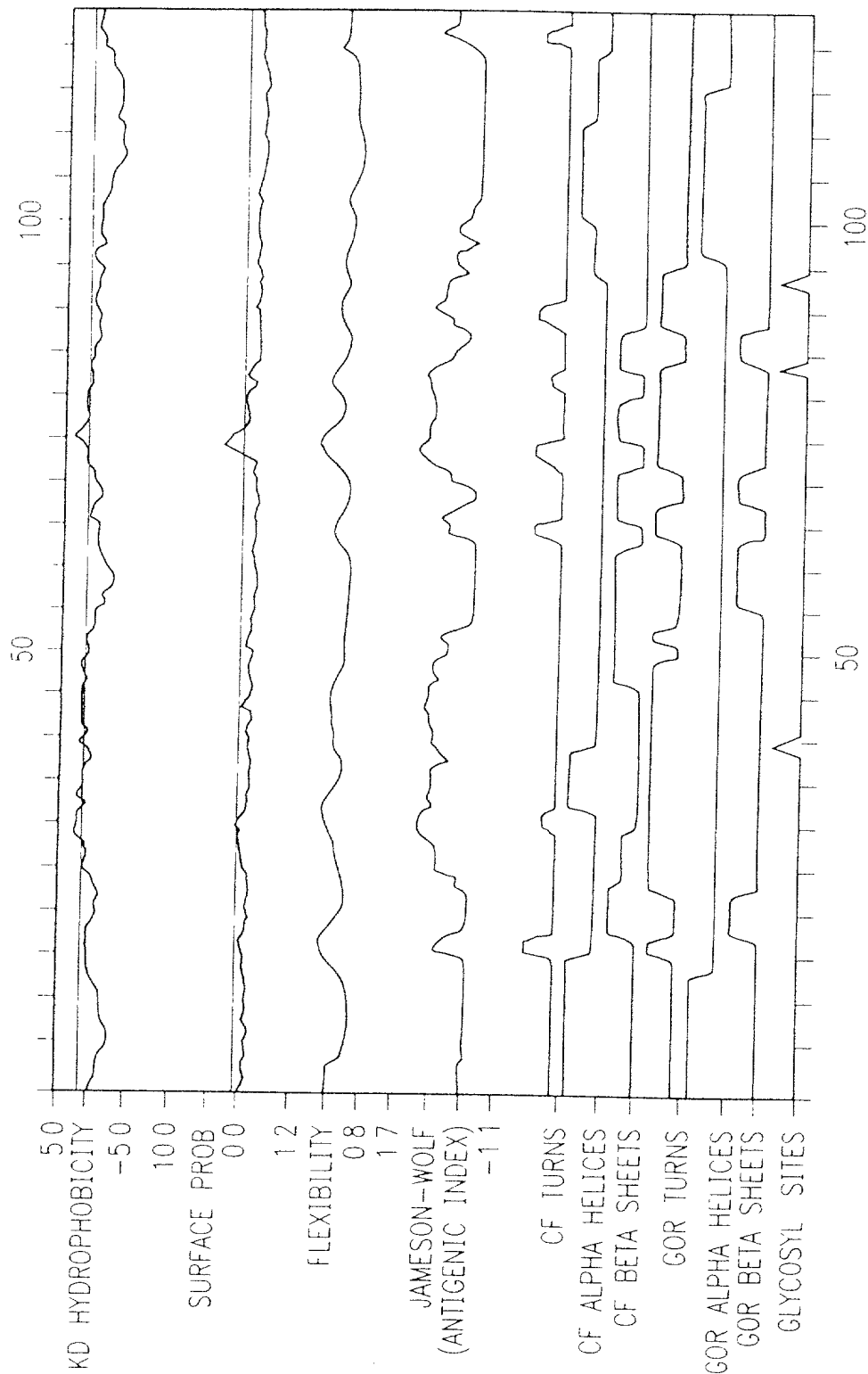
1 ATGAAGACAGTTTTTTTTATCCTGCTGGCCACCTACTTAGCCCTGCATCCAGGTGCTGCT  
 -----+-----+-----+-----+-----+-----+ 60  
 TACTTCTGTCAAAAAAATAGGACGACCGGTGGATGAATCGGGACGTAGGTCCACGACGA  
  
 M K T V F F I L L A T Y L A L H P G A A  
  
 61 CTGCAGTGCTATTCATGCACAGCACAGATGAACAACAGAGACTGTCTGAATGTACAGAAC  
 -----+-----+-----+-----+-----+-----+ 120  
 GACGTCACGATAAGTACGTGTCGTGCTACTTGTGTCTCTGACAGACTTACATGTCTTG  
  
 L Q C Y S C T A Q M N N R D C L N V Q N  
  
 121 TGCAGCCTGGACCAGCACAGTTGCTTTACATCGCGCATCCGGGCCATTGGACTCGTGACA  
 -----+-----+-----+-----+-----+-----+ 180  
 ACGTCGGACCTGGTCGTGTCAACGAAATGTAGCGGTAGGCCCGGTAACCTGAGCACTGT  
  
 C S L D Q H S C F T S R I R A I G L V T  
  
 181 GTTATCAGTAAGGGCTGCAGCTCACAGTGTGAGGATGACTCGGAGAACTACTATTTGGGC  
 -----+-----+-----+-----+-----+-----+ 240  
 CAATAGTCATTCCCGACGTCGAGTGTCACTCCTACTGAGCCTCTTGATGATAAACCCG  
  
 V I S K G C S S Q C E D D S E N Y Y L G  
  
 241 AAGAAGAACATCACGTGCTGCTACTCTGACCTGTGCAATGTCAACGGGGCCACACCCTG  
 -----+-----+-----+-----+-----+-----+ 300  
 TTCTTCTGTAGTGACGACGATGAGACTGGACACGTTACAGTTGCCCCGGGTGTGGGAC  
  
 K K N I T C C Y S D L C N V N G A H T L  
  
 301 AAGCCACCCACCCCTGGGGCTGCTGACCGTGTCTGCAGCCTGTTGCTGTGGGGCTCC  
 -----+-----+-----+-----+-----+-----+ 360  
 TTCGGTGGGTGGTGGGACCCGACGACTGGCACGAGACGTCGGACAACGACACCCCGAGG  
  
 K P P T T L G L L T V L C S L L L W G S  
  
 361 AGCCGTCTGTAGGCTCTGGGAGAGCCTACCATAGCCCGATTGTGAAGGGATGAGCTGCAC  
 -----+-----+-----+-----+-----+-----+ 420  
 TCGGCAGACATCCGAGACCCTCTCGGATGGTATCGGGCTAACACTTCCCTACTCGACGTG  
  
 S R L \*  
  
 421 TCCACCCACCCACACAGG  
 -----+-----+ 441  
 AGGTGGGGTGGGGGTGTGTCC

05431.07501

FIG. 3

1	M	K	I	F	L	P	V	L	L	A	A	L	L	G	V	E	R	A	S	S	hSCA-2
1	M	K	A	V	L	L	A	L	L	M	A	G	L	A	L	Q	P	G	T	A	hPSCA
1	M	K	T	V	L	F	L	L	L	A	T	Y	L	A	L	H	P	G	A	A	mPSCA
21	L	M	C	F	S	C	L	N	Q	K	S	N*	L	Y	C	L	K	P	T	I	
21	L	L	C	Y	S	C	K	A	Q	V	S	N*	E	D	C	L	Q	V	E	N*	
21	L	Q	C	Y	S	C	T	A	Q	M	N	N*	R	D	C	L	N	V	Q	N*	
41	C	S	D	Q	D	N	Y	C	V	T	V	S	A	S	A	G	I	G	N	L	
41	C	T	Q	L	G	E	Q	C	W	T	A	R	I	R	A	V	G	L	L	T	
41	C	S	L	D	Q	H	S	C	F	T	S	R	I	R	A	I	G	L	V	T	
61	V	T	F	G	H	S	L	S	K	T	C	S	P	A	C	P	I	P	E	G	
61	V	-	-	-	-	-	-	I	S	K	G	C	S	L	N	C	V	D	D	S	Q
61	V	-	-	-	-	-	-	I	S	K	G	C	S	S	Q	C	E	D	D	S	E
81	V	N	V	G	V	A	S	M	G	I	S	C	C	Q	S	F	L	C	N*	F	
76	D	Y	Y	V	G	K	K	-	N*	I	T	C	C	D	T	D	L	C	N*	A	
76	N	Y	Y	L	G	K	K	-	N*	I	T	C	C	Y	S	D	L	C	N*	V	
101	S	A	A	D	G	G	L	R	A	S	V	T	L	L	G	A	G	L	L	L	
95	S	G	A	H	A	L	Q	P	A	A	A	I	L	A	L	L	P	A	L	G	
95	N	G	A	H	T	L	K	P	P	T	T	L	G	L	L	T	V	L	C	S	
121	S	L	L	P	A	L	L	R	F	G	P										
115	L	L	L	W	G	P	G	Q	L	-	-										
115	L	L	L	W	G	S	S	R	L	-	-										

FIG. 4



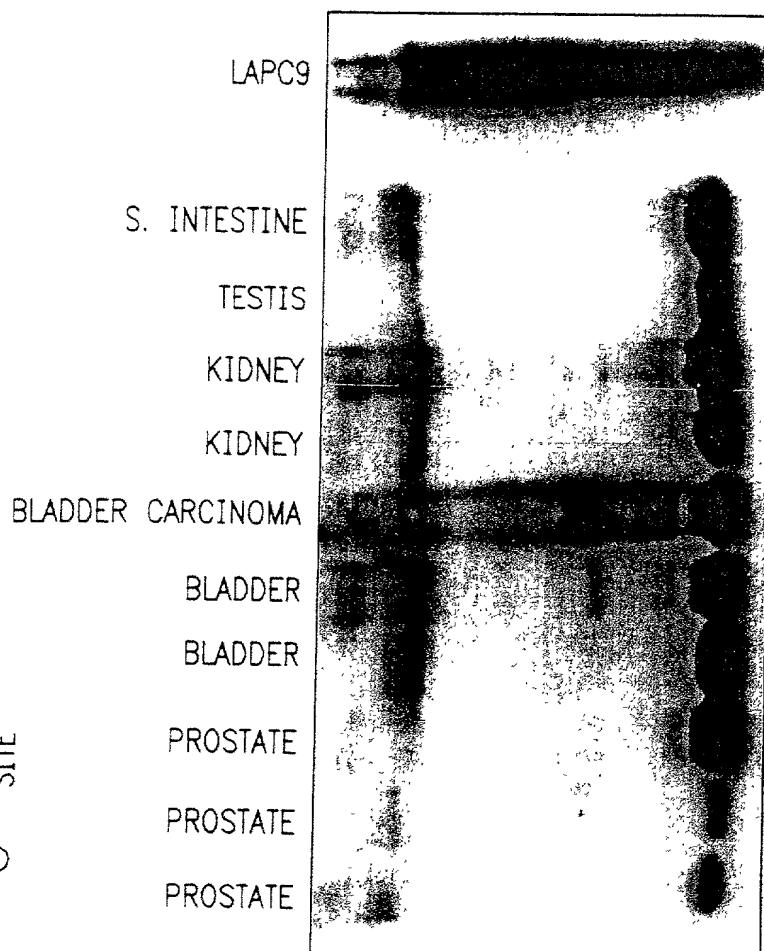
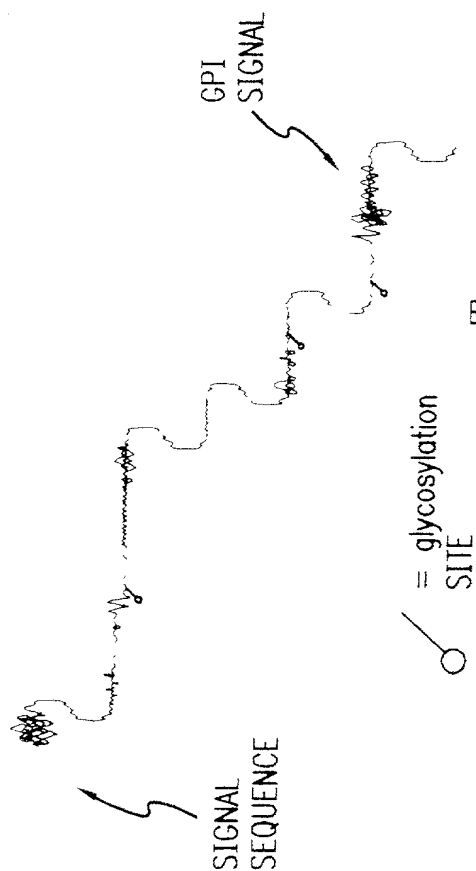


FIG. 6

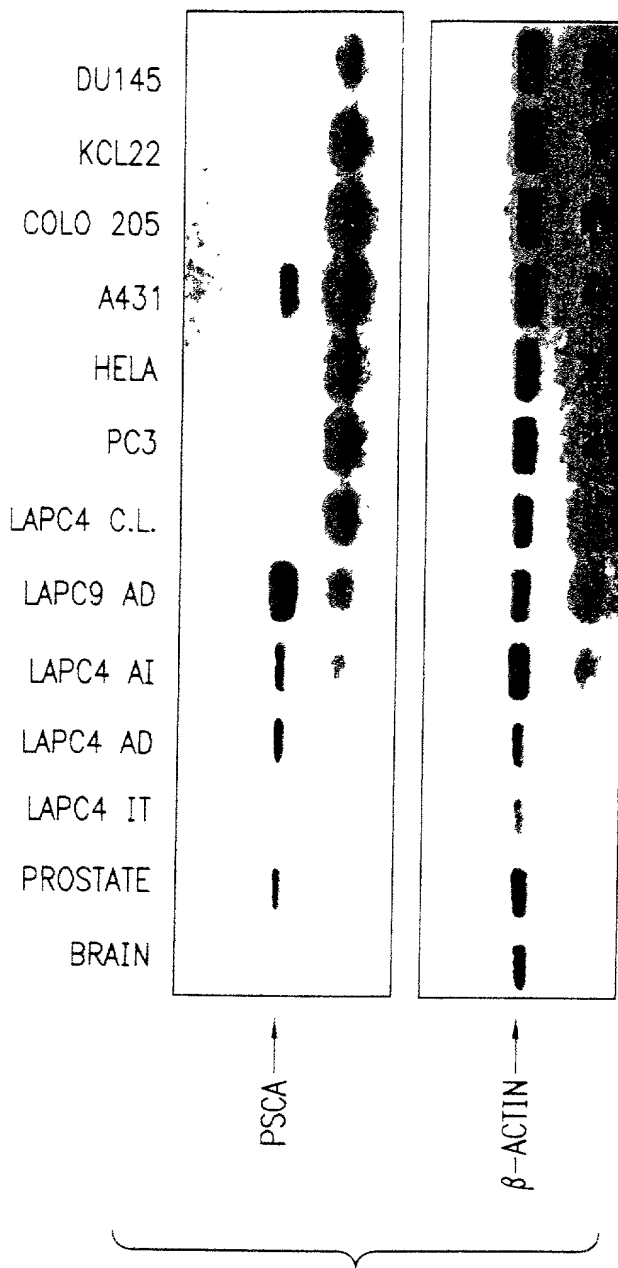
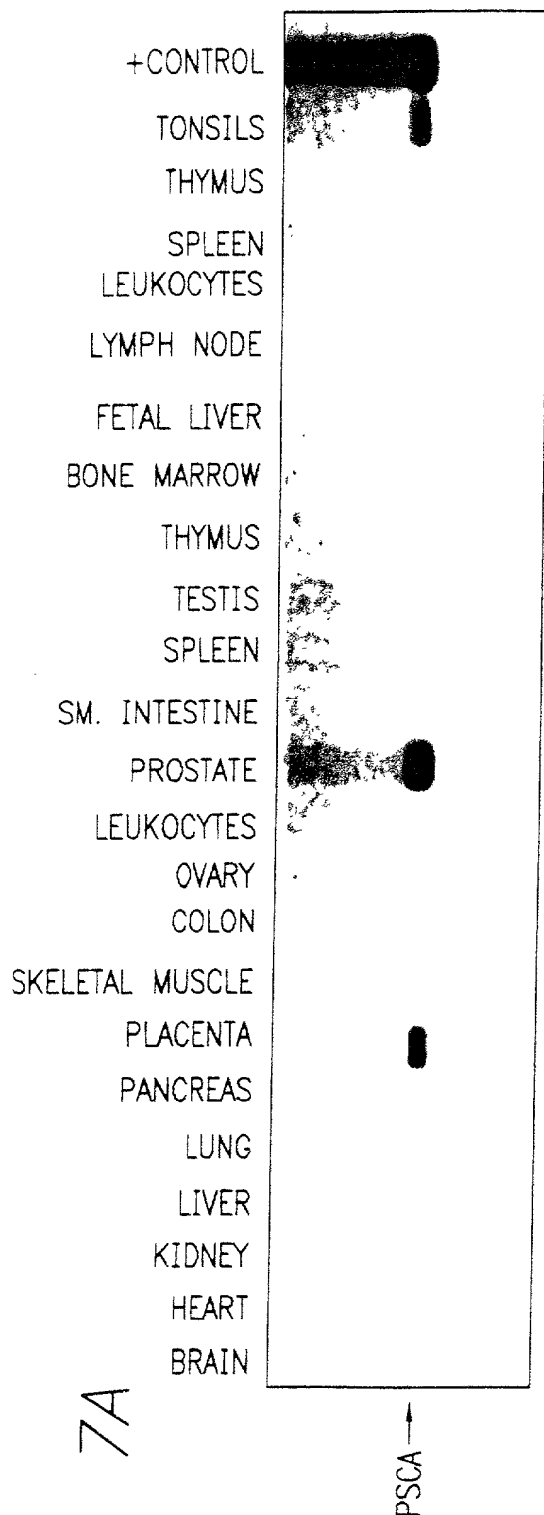


FIG. 8A

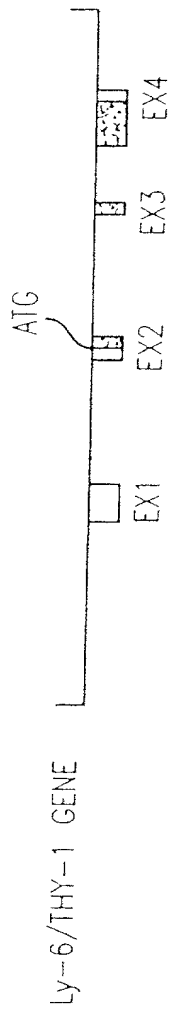


FIG. 8B

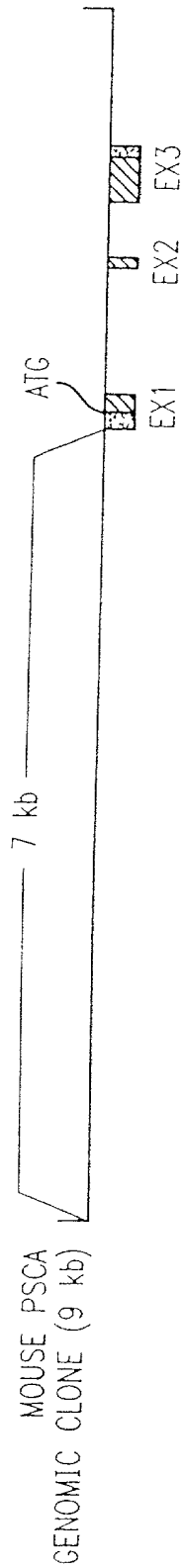
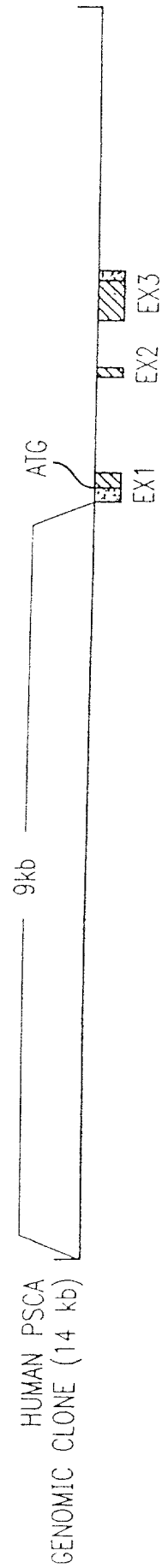


FIG. 8C



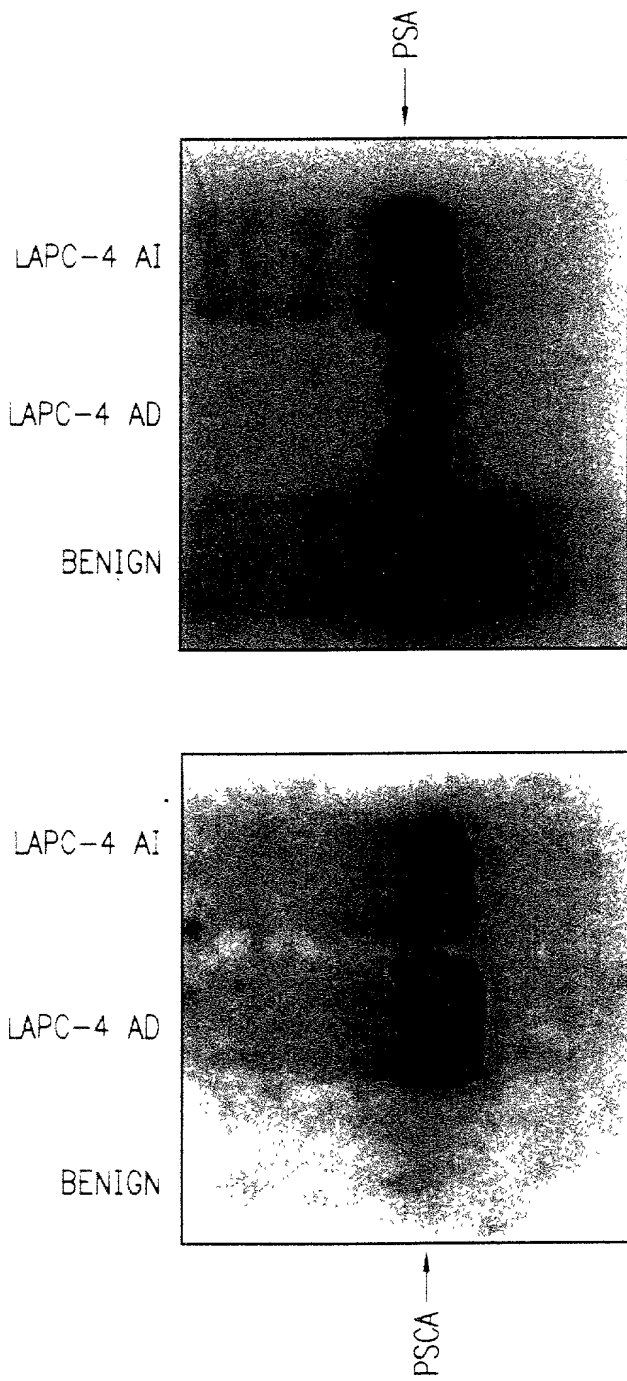
[illegible]

FIG. 9A



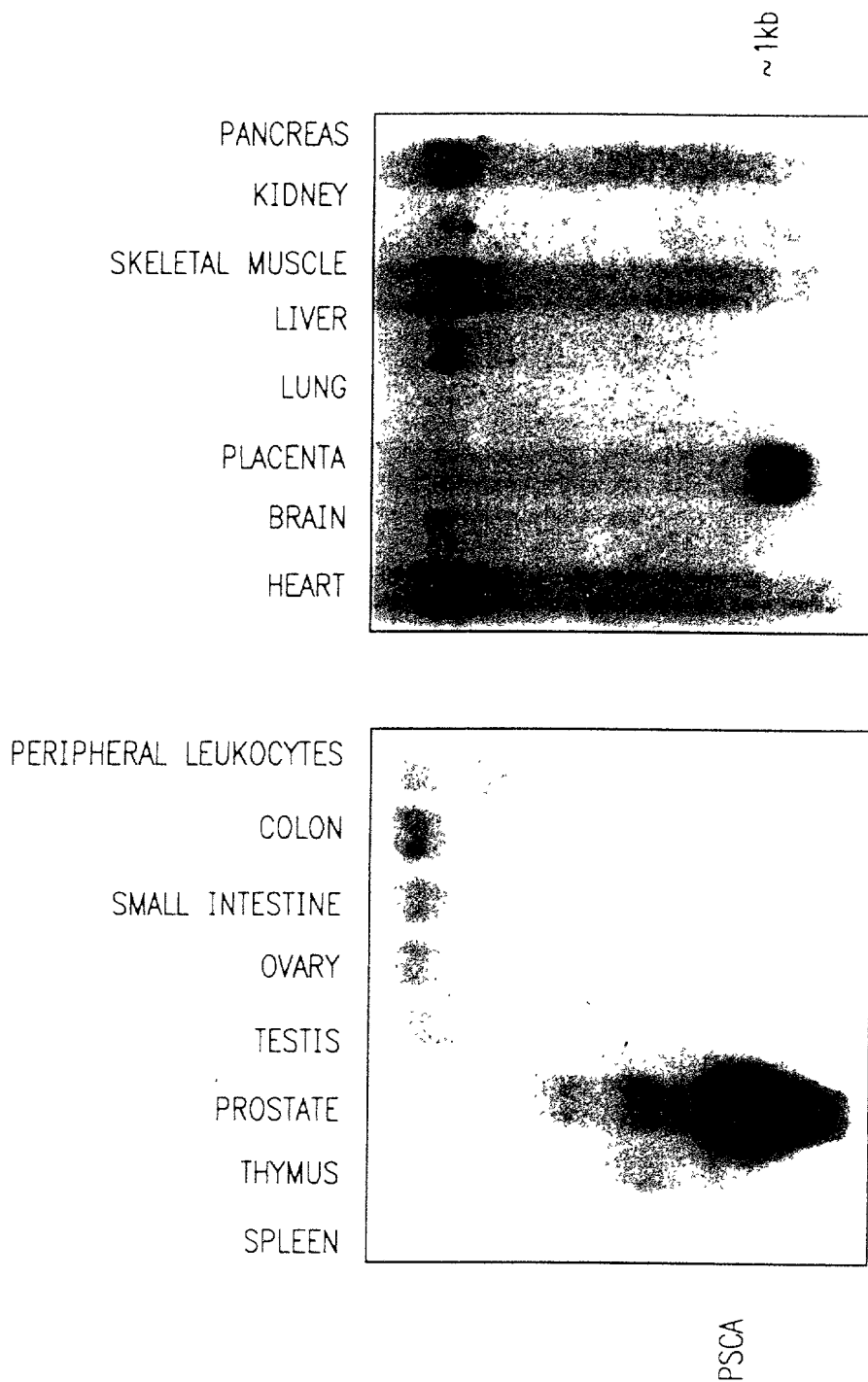


FIG. 9B

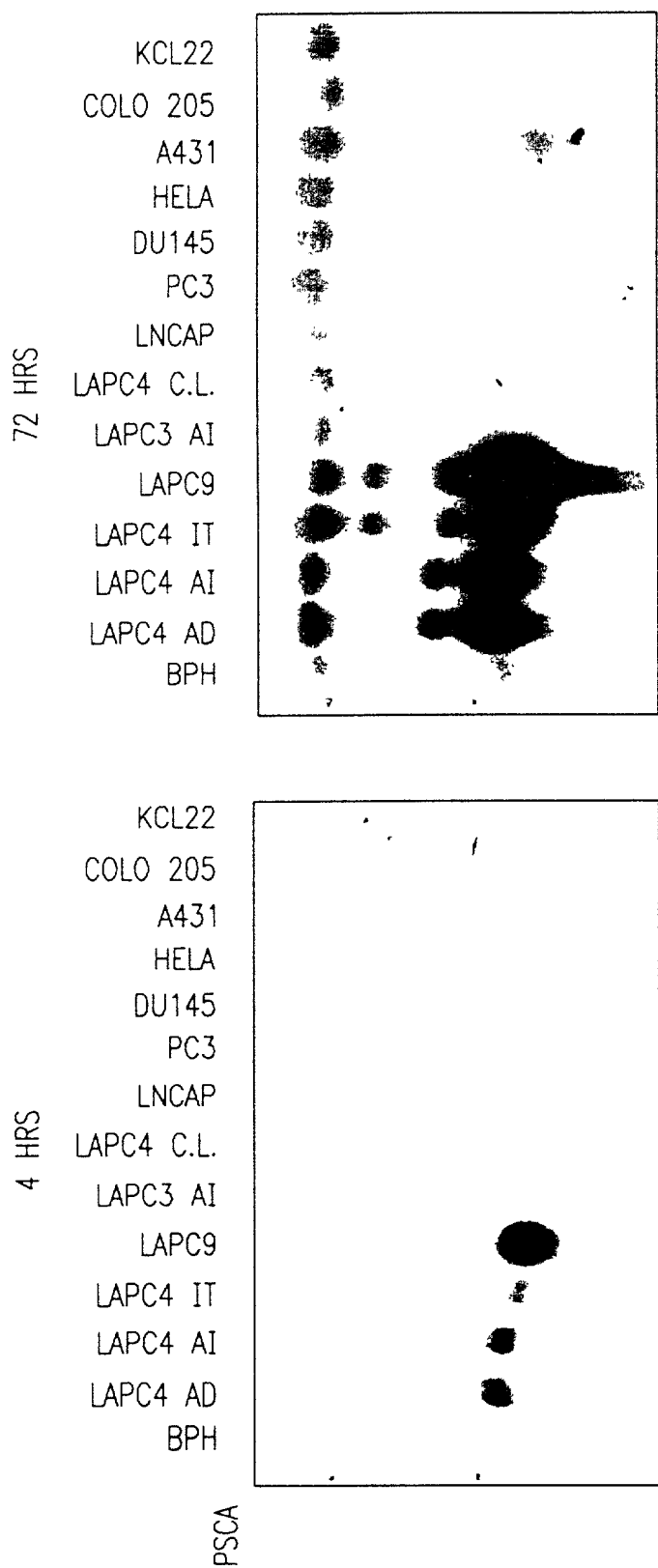
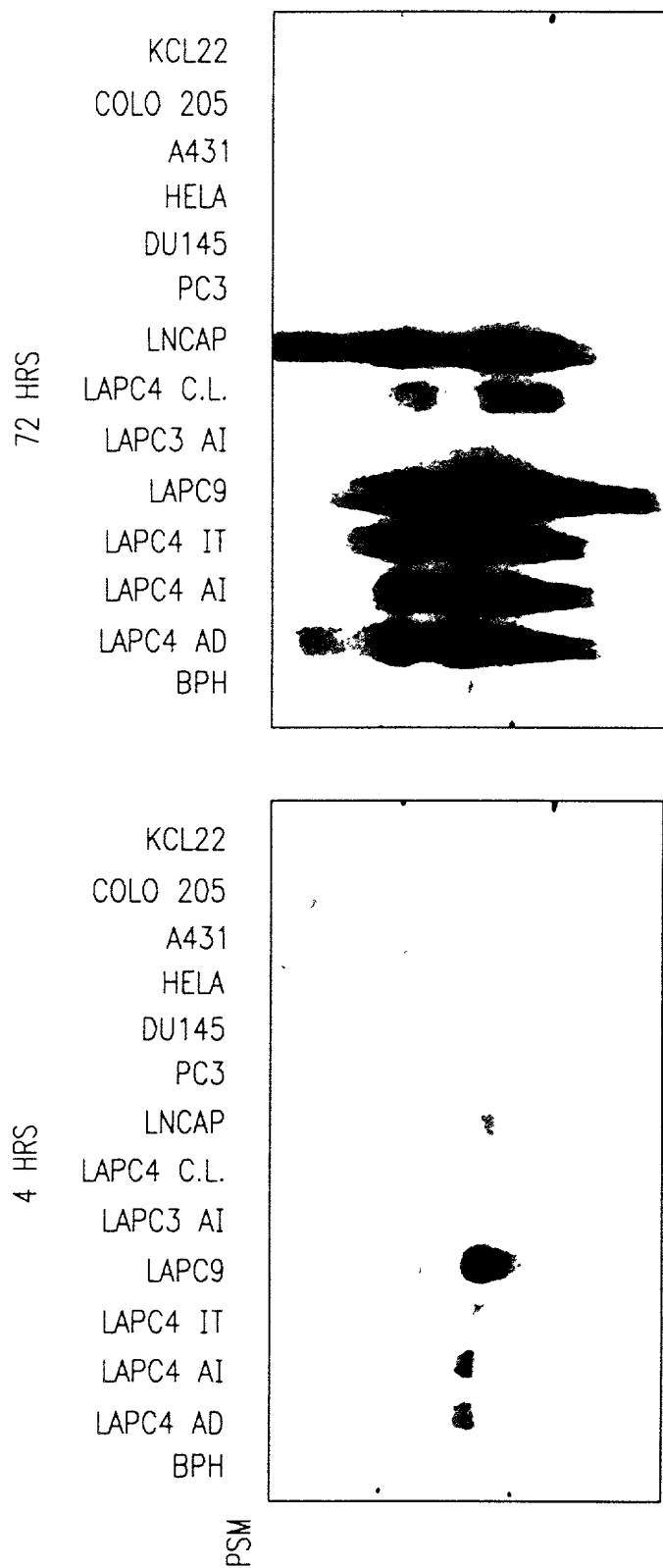


FIG. 10A



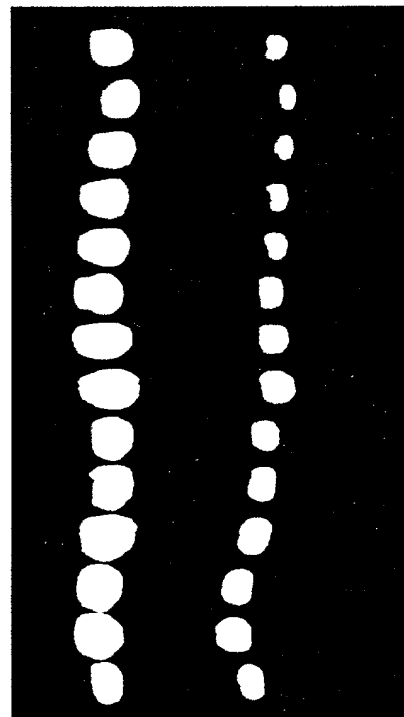
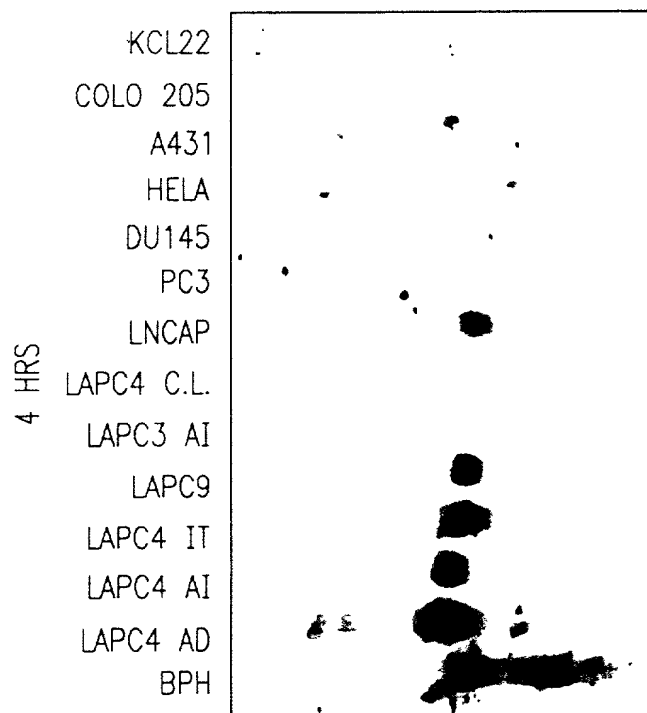
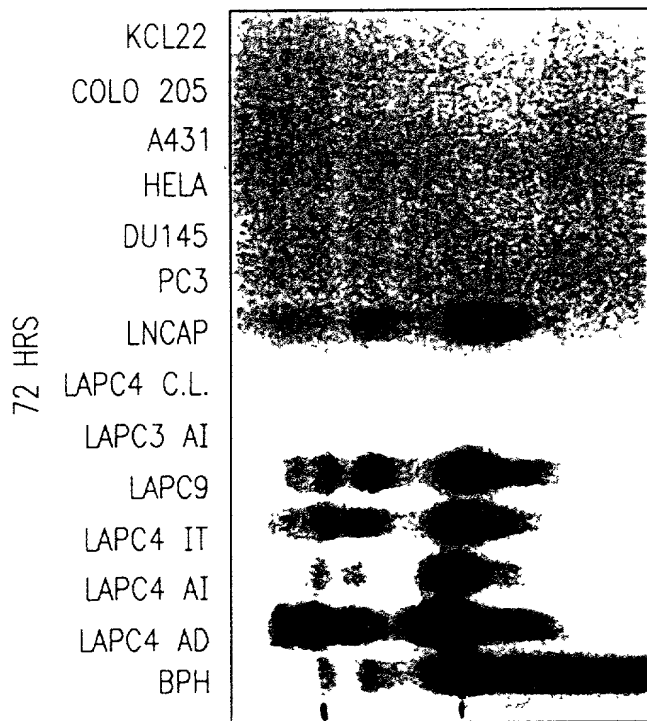


FIG. 10C

FIG. 11A



FIG. 11B

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09854811.072501



FIG. 11C

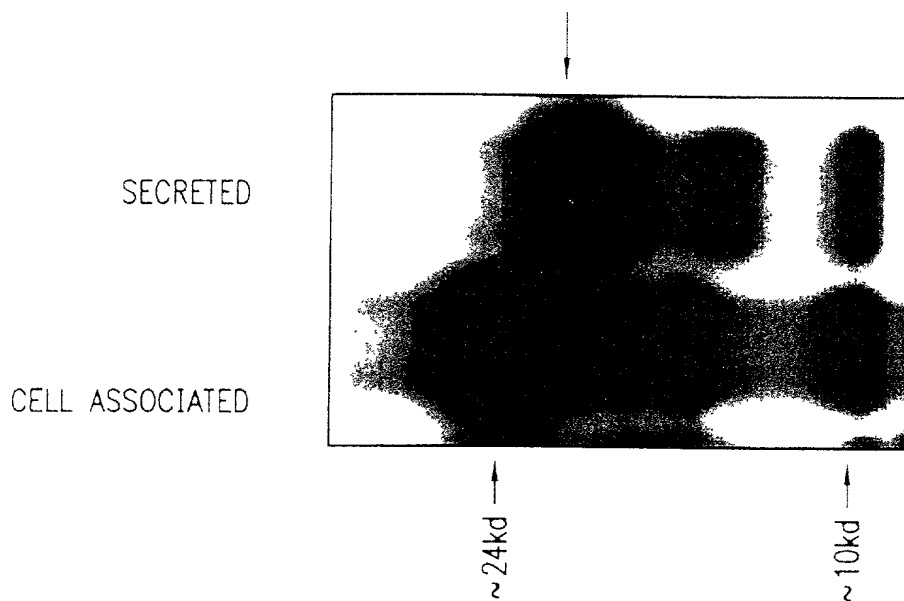
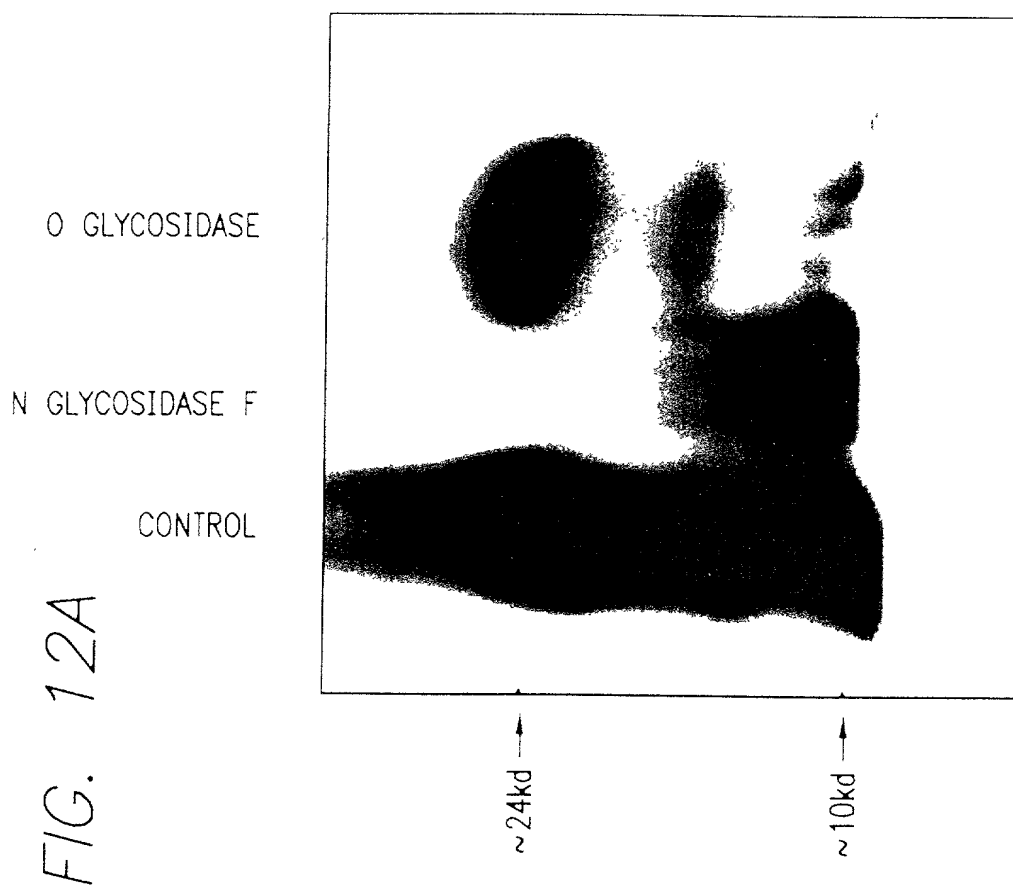


FIG. 12B

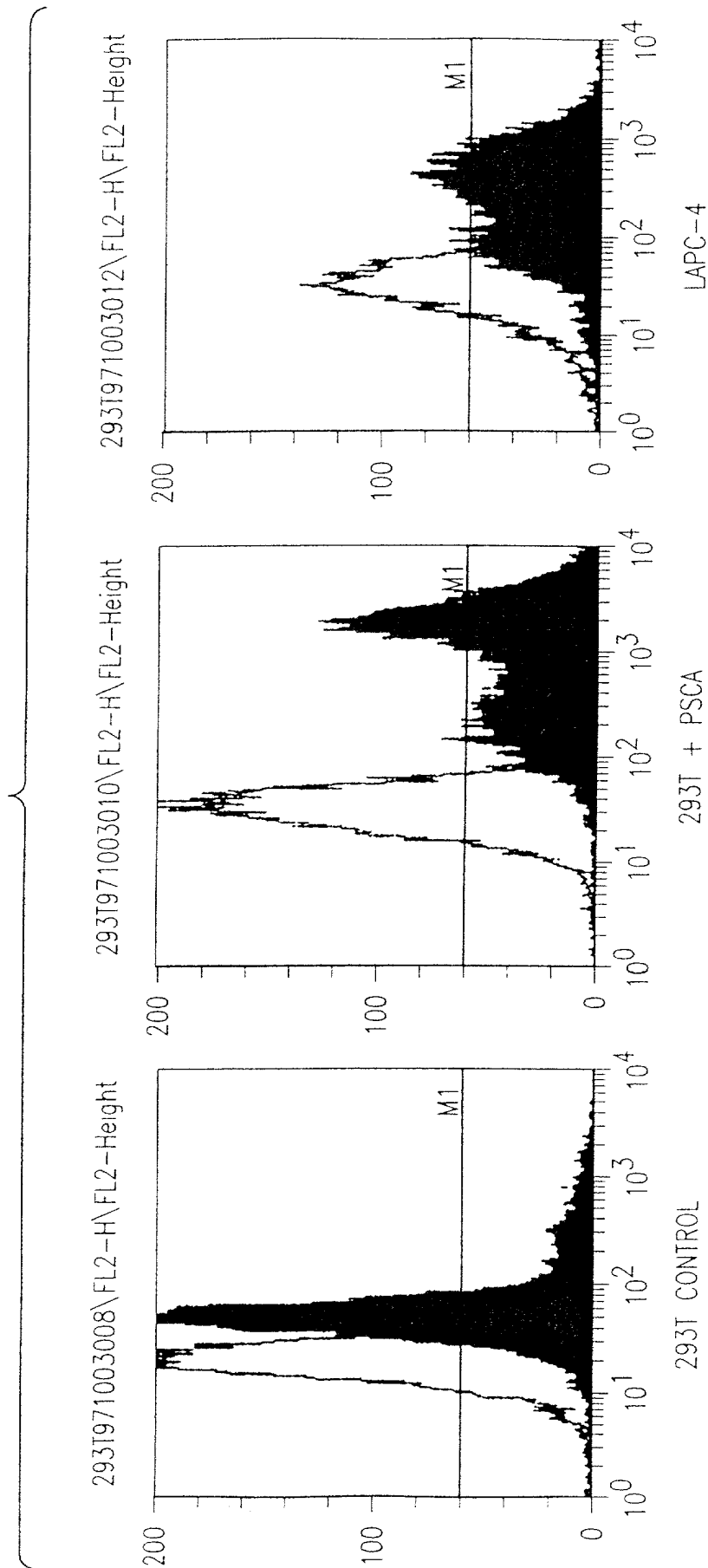


FIG. 12C



FIG. 13

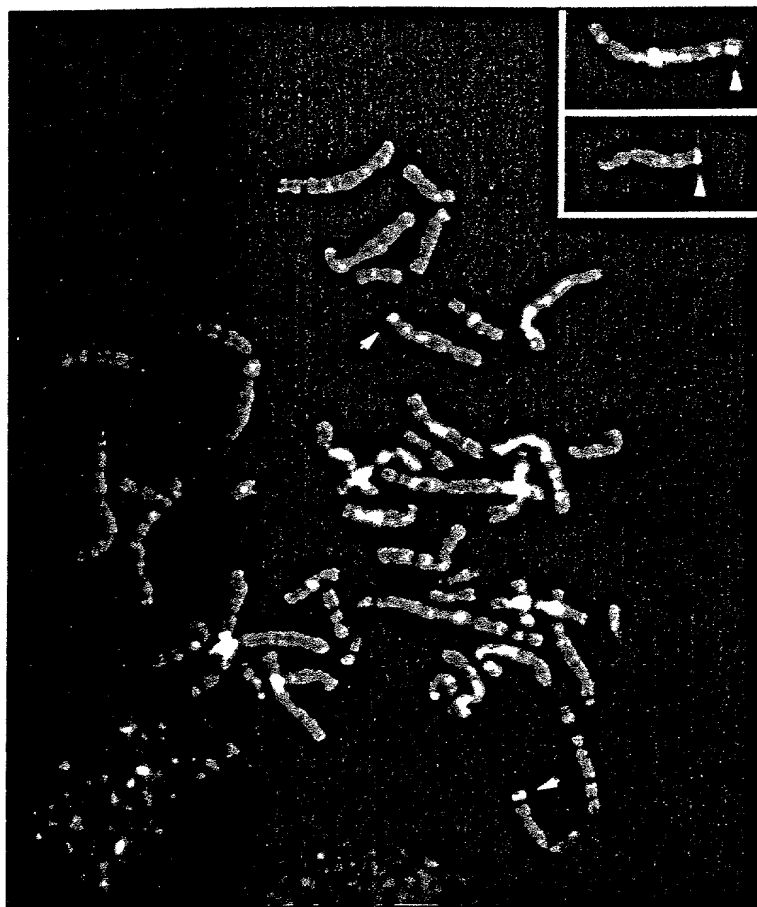


FIG. 14A

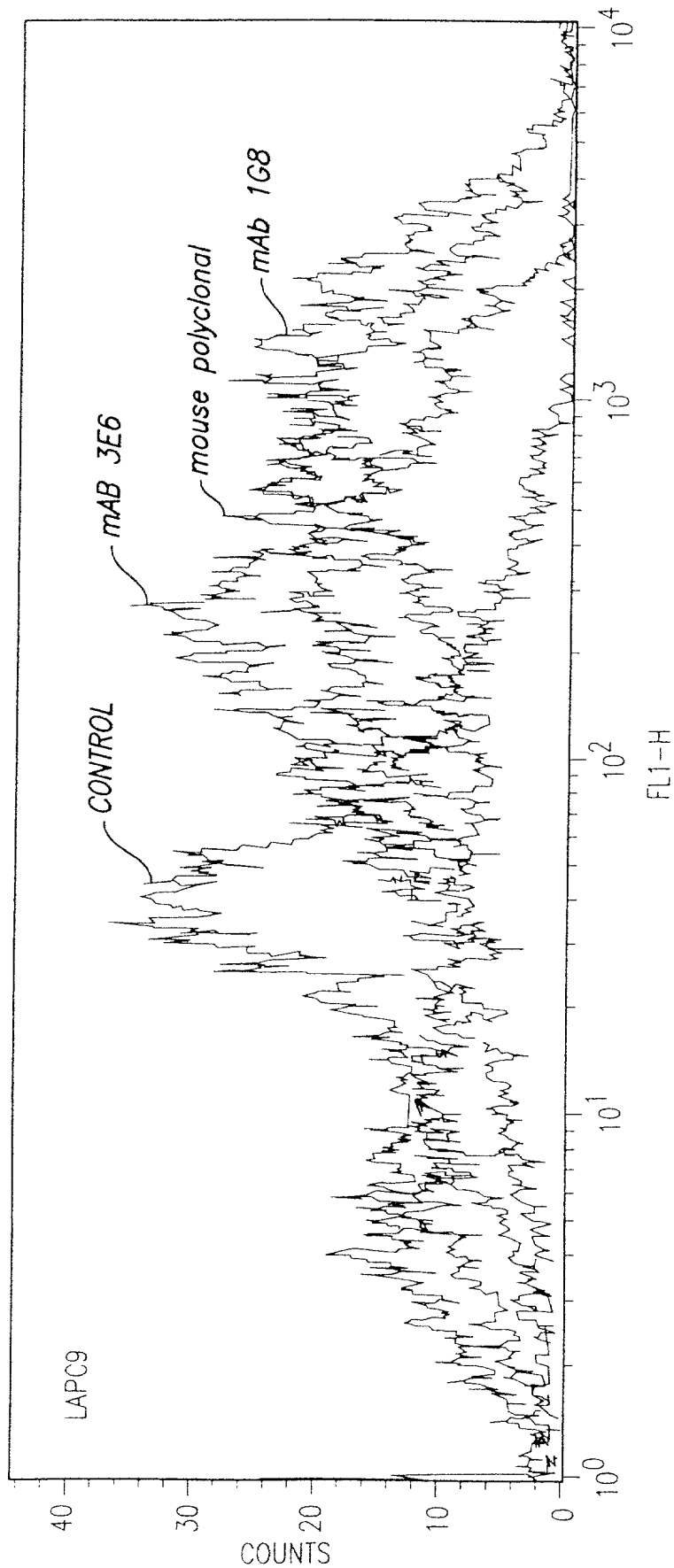


FIG. 14B

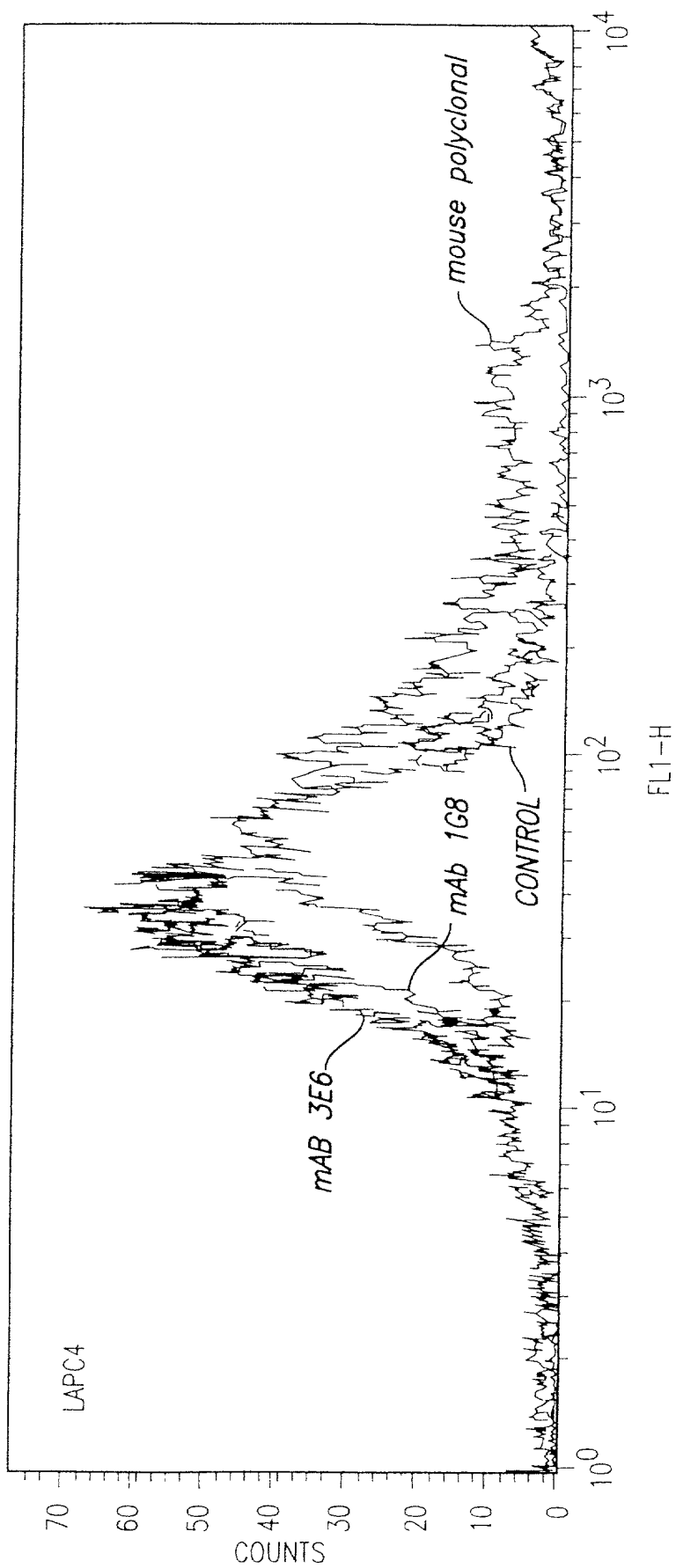
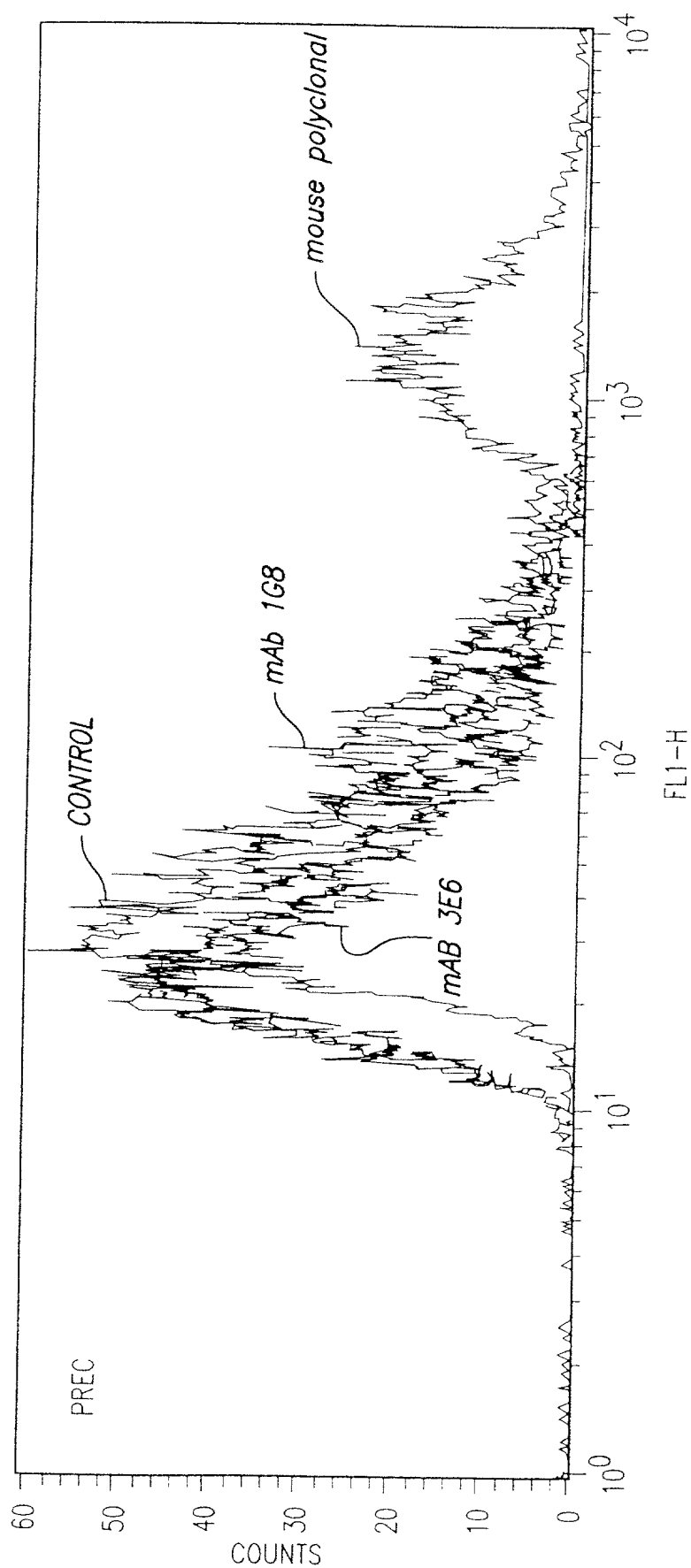


FIG. 14C



mAb	ISOTYPE	EPIIOPE MAP			
		FL (18-98)	N (2-50)	M (46-109)	C (85-123)
1G8	IgG1 k	2.039	0.007	0.628	0.000
2H9	IgG1 k	1.318	0.863	0.032	0.021
3C5	IgG2a k	2.893	1.965	0.016	0.005
3E6	IgG3 k	0.328	0.024	0.069	0.370
4A10	IgG2a k	2.039	1.315	0.000	0.014
2A2	IgG2a k	1.366	0.733	0.010	0.003
3G3	IgG2a k	2.805	1.731	0.004	0.000

FIG. 15A

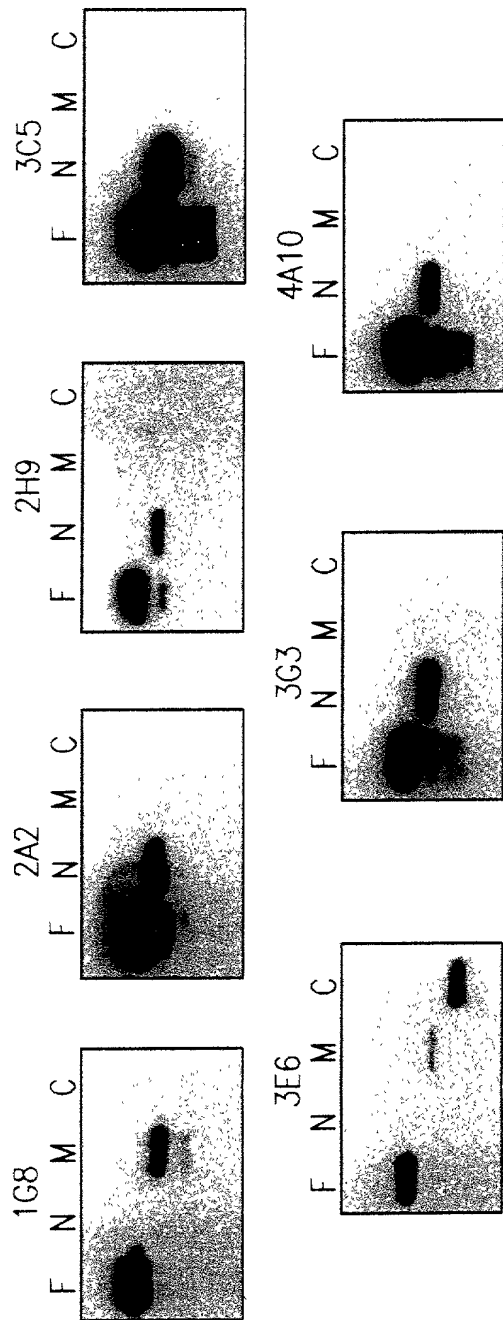


FIG. 15B

hSCA-2  
hPSCA  
mPSCA

1	M K I F L P V L A A L G V E R A S S
1	M K A V L L A L L M A G L A L Q P C T A
1	M K T V L F L L E A T Y L A L H P C A A
21	L M C F S C L N O K S N* L Y C L K P T I
21	L L C X S C K A Q V S N* E D C L Q N V E N*
21	L L Q C Y S C T A Q M N N* R D C L V Q N*
41	C S D Q D N Y C V T V S A S A G I G N L
41	C T Q L G E Q C W T A R U R A V C L L T
41	C S L D Q H S C F T S R I R A I G L V
61	V T F G H S L S K T C S P A C V P I P E G
61	V - - - - I S X G C S L N C V D D S Q Q
61	V - - - - I S K G C S S Q C E D D S E
81	V N V G V A S M G L S C C Q Q S F E C N*
76	D X Y V C K K - N I T C G C D T D L C N*
76	N X Y L G K K - N I T C C S D L C N*
101	S A A D G G L R A S V T L L G A G L L L
95	S G A H A L Q P A A A I L A L L P A L G
95	N C A H T L K P P T T L G L L T V L C S
121	S L L P A L L R F G P
115	L L W G P G Q L - -
115	L L W G S S R L - -

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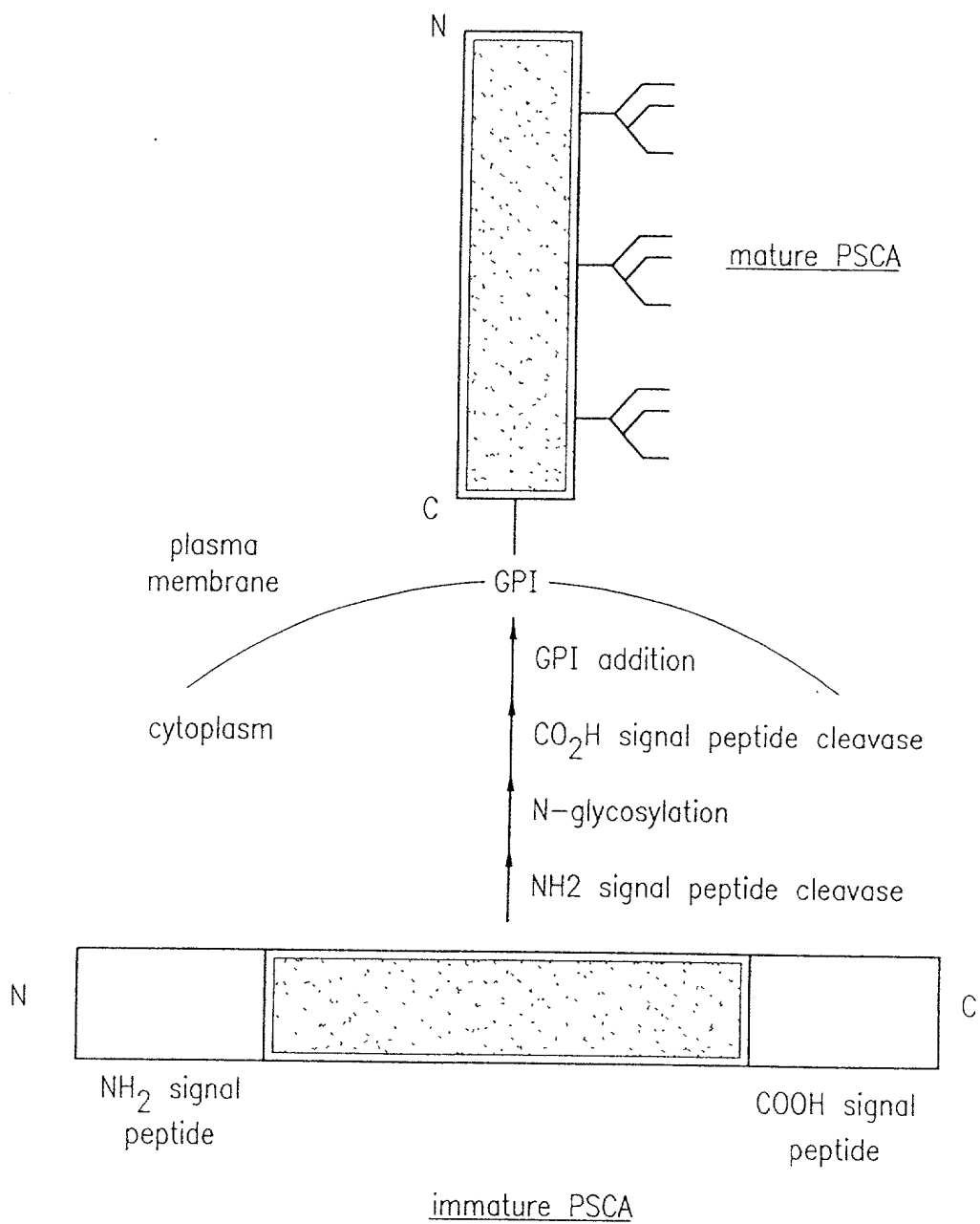
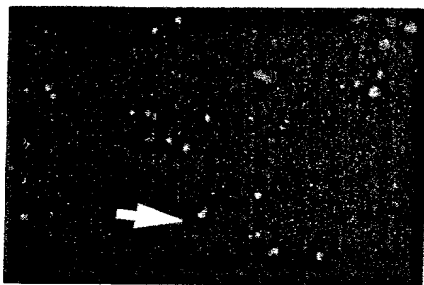


FIG. 16B

FIG. 17

GAIN CHROMOSOME 8

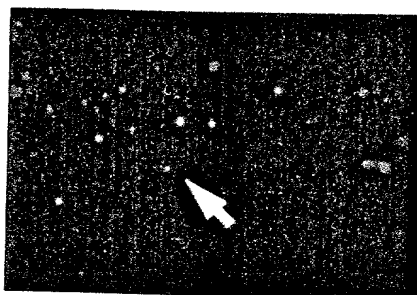


#34 c-myc

#34 PSCA



AMPLIFICATION



#75 c-myc

#75 PSCA

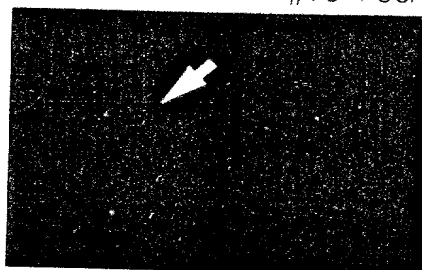
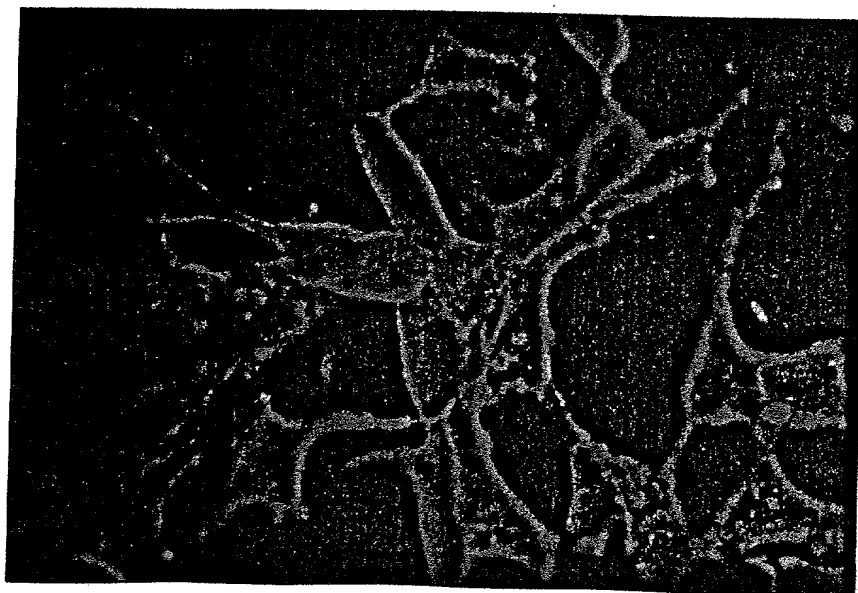


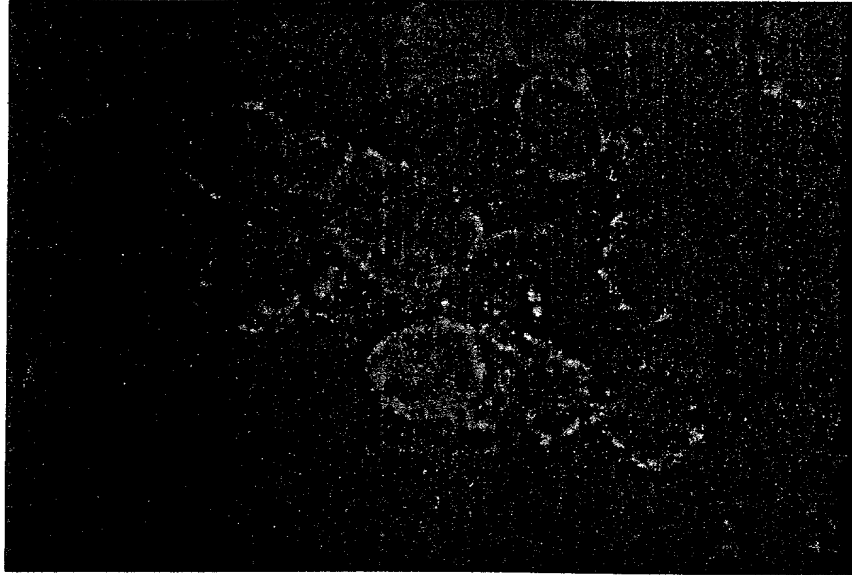
FIG. 18



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T05270" T845860



*FIG. 19*

*FIG. 20*

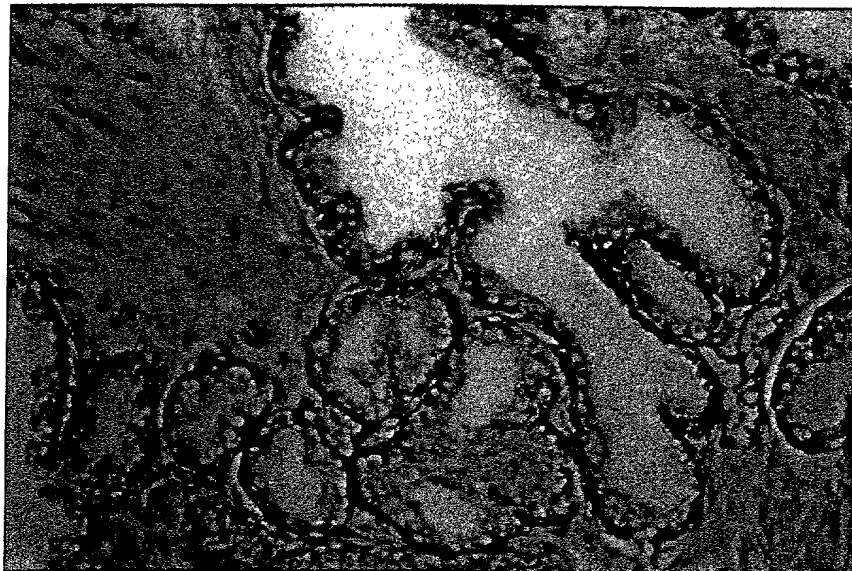
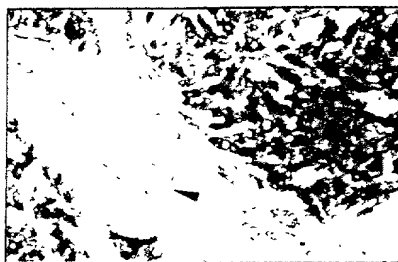
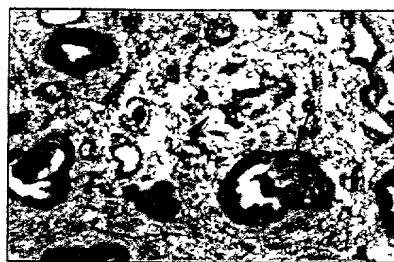


FIG. 21

PSCA IMMUNOSTAINING OF PRIMARY TUMORS



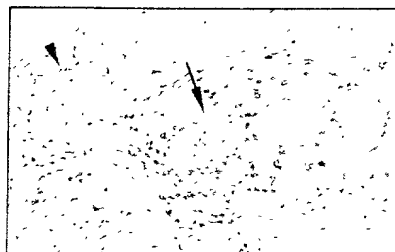
patient 1:mAb 1G8



patient 2:mAb 1G8

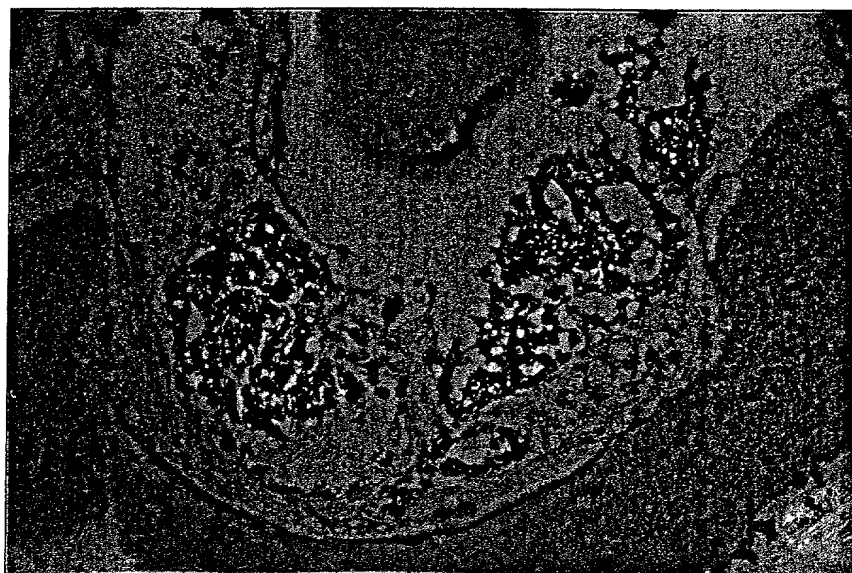


patient 3:mAb 1G8

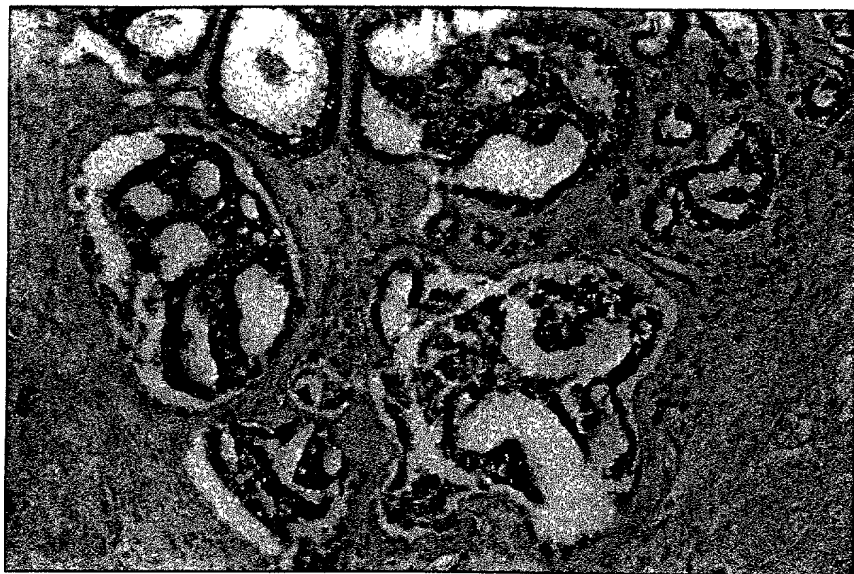


patient 4:mAb 3E6

FIG. 22



09654811.072501



*FIG. 23*

*FIG. 24*



005441 0220  
"05240" 11845860

FIG. 25

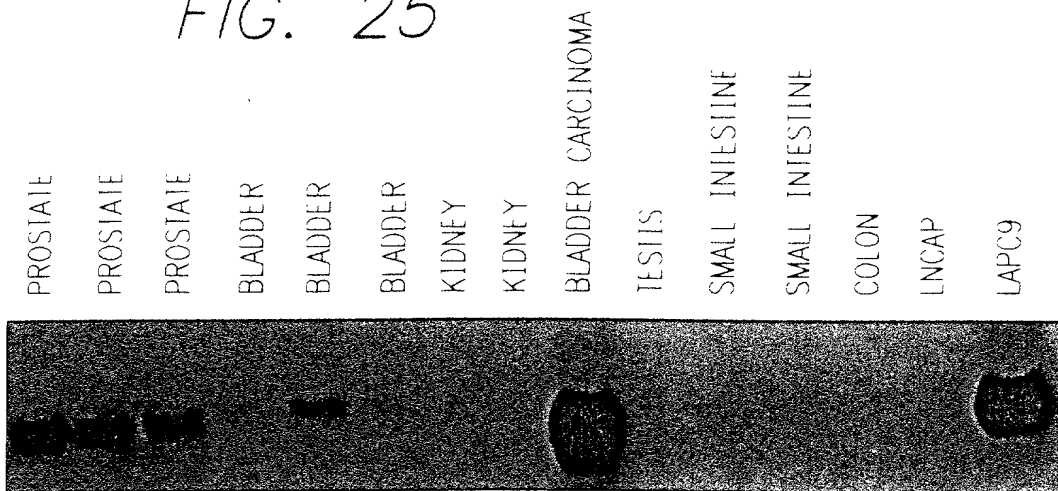


FIG. 26

09854811.072501

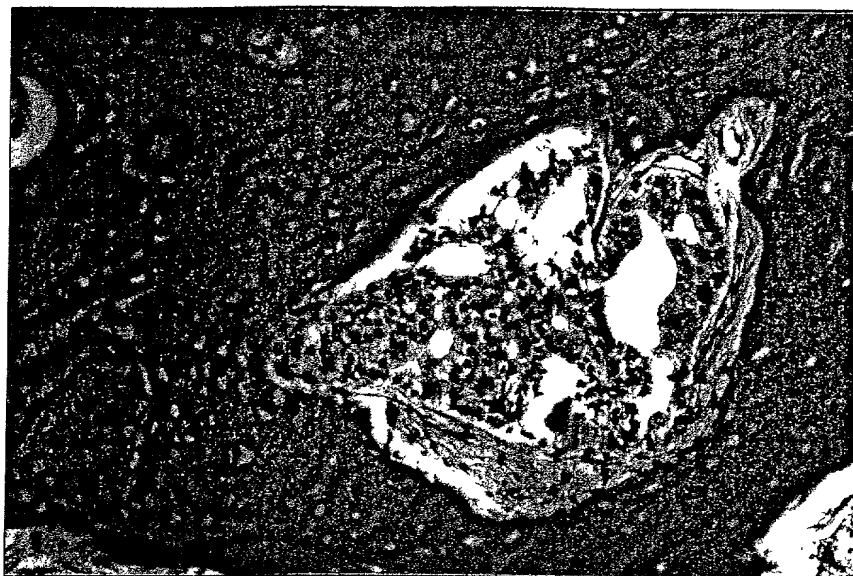
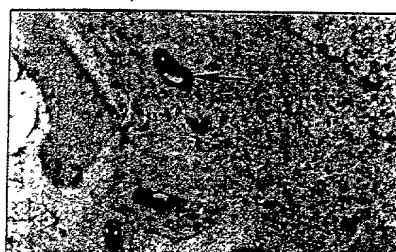
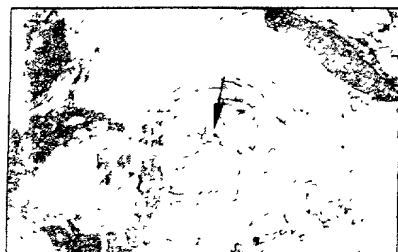
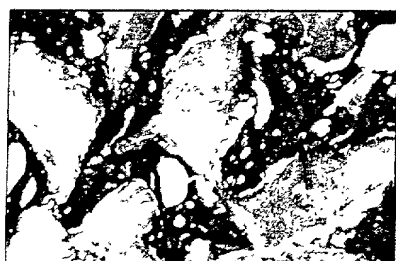


FIG. 27

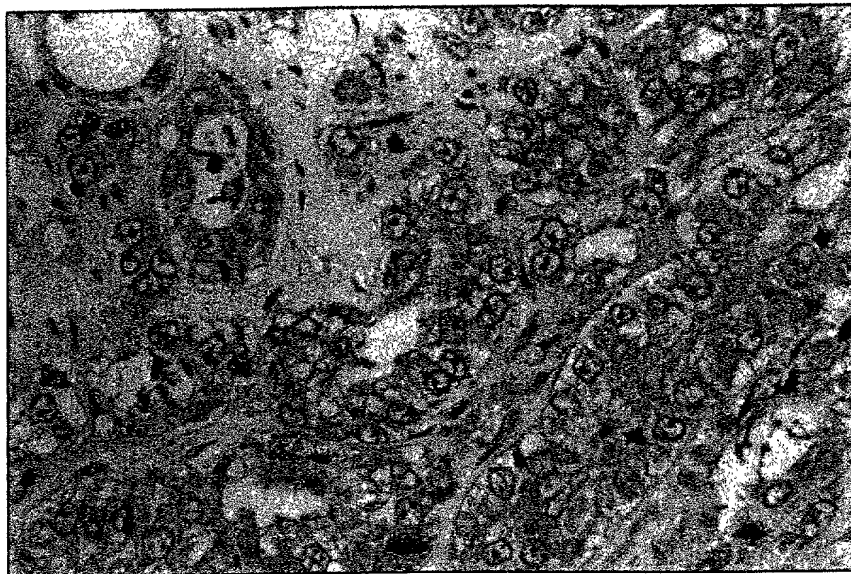


Patient 5: H and E  
and mAb 1G8



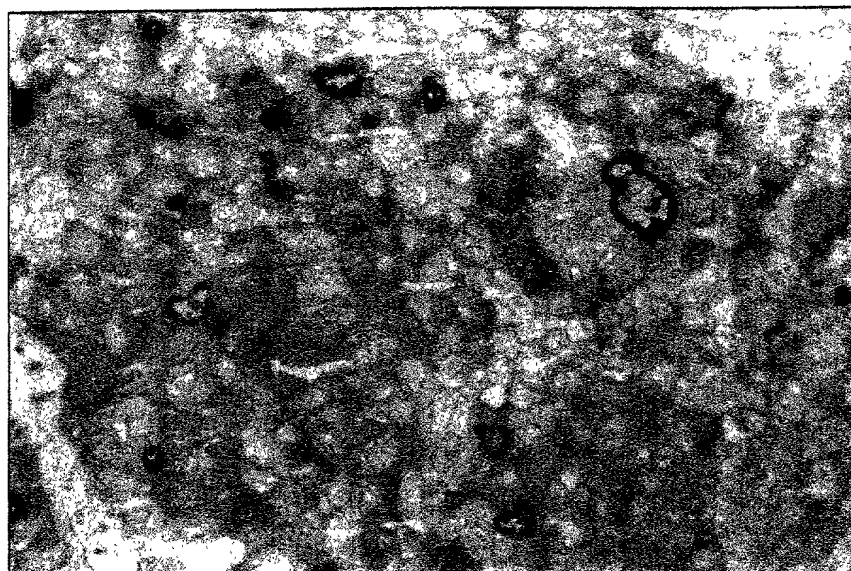
Patient 4: H and E  
and mAb 3E6

FIG. 28

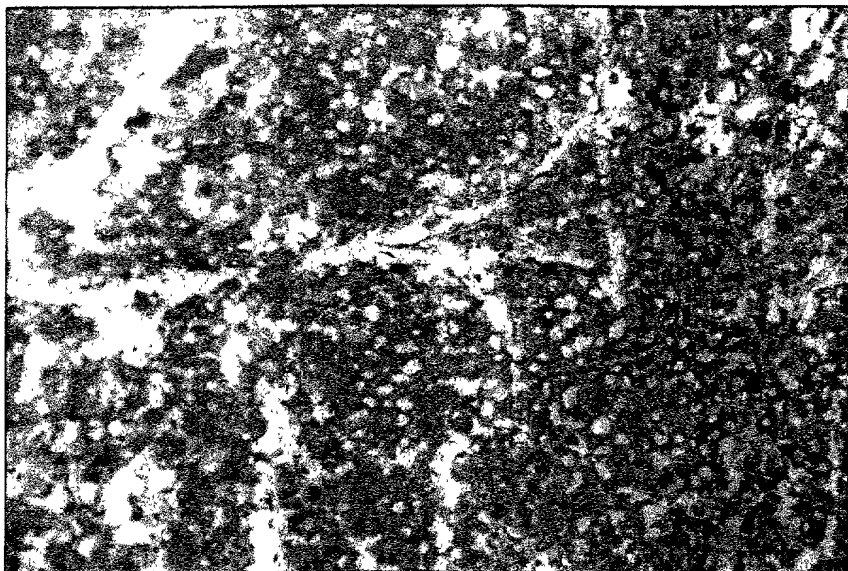


*FIG. 29*

*FIG. 30*



09854811 072504  
T05270 T1845860



*FIG. 31*

*FIG. 32*

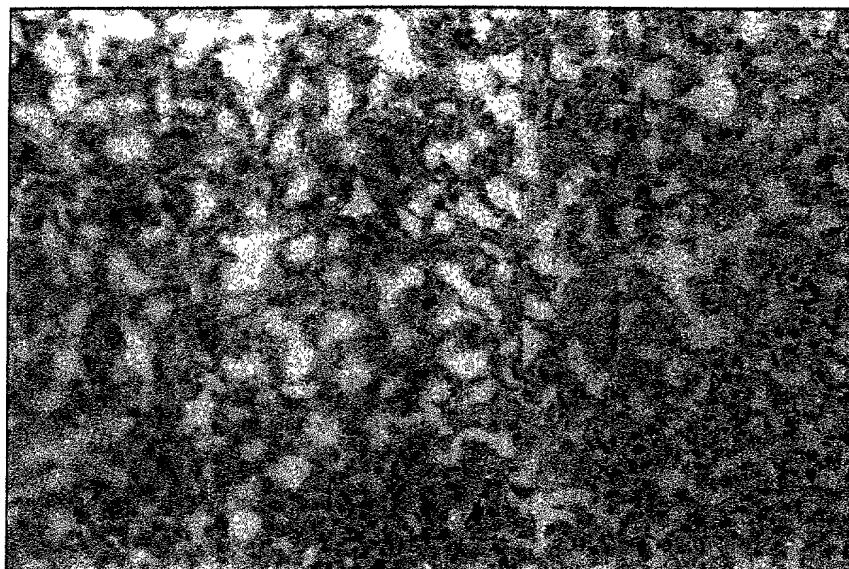


FIG. 33

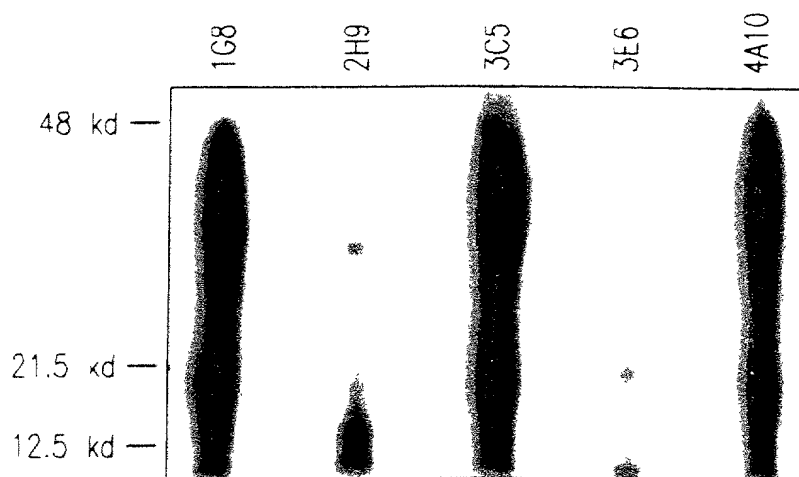
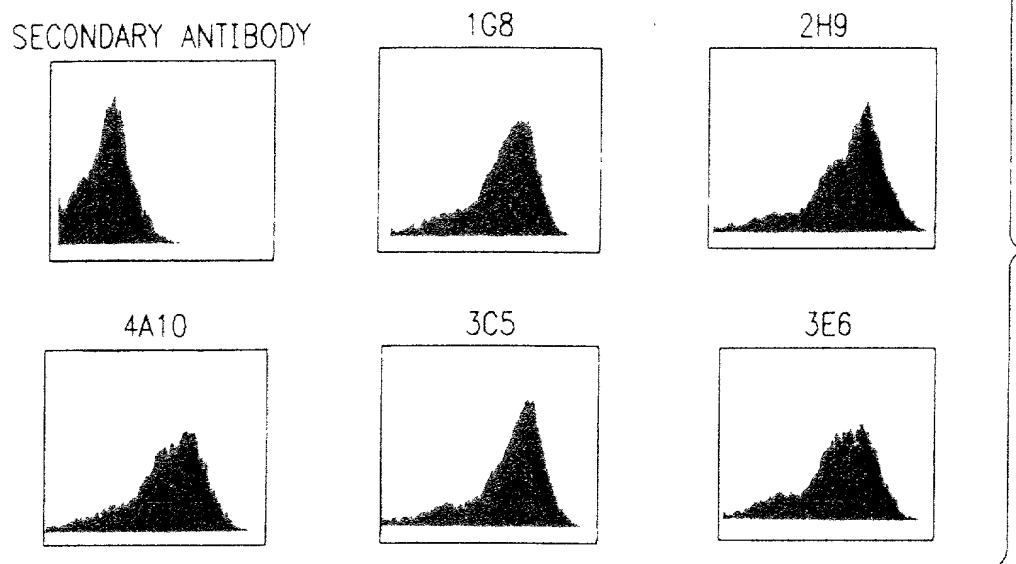


FIG. 34



FIG. 35

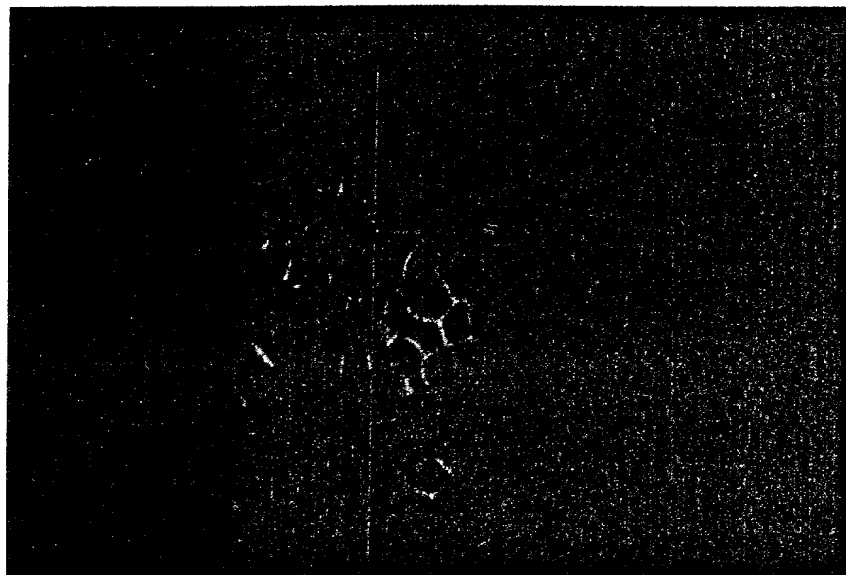
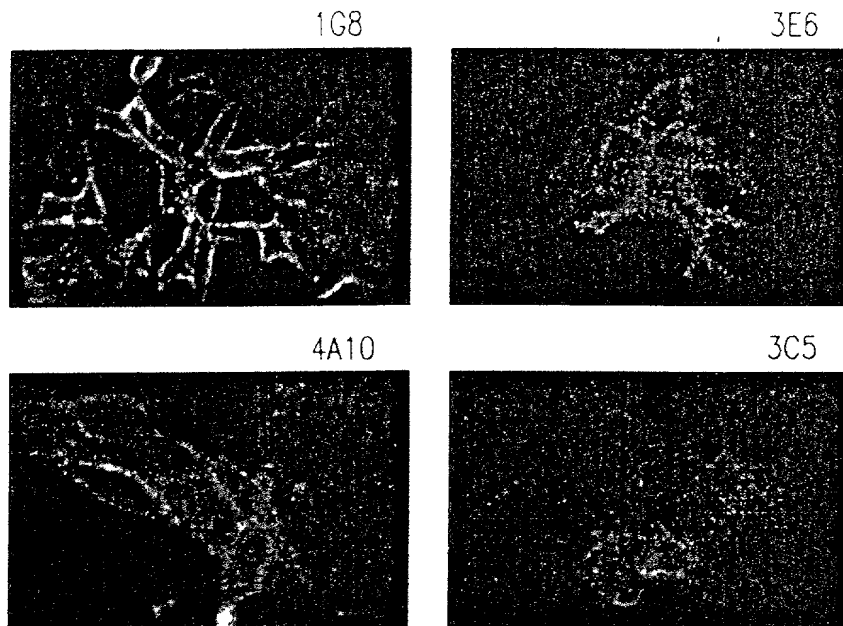


FIG. 36

09654811.072501

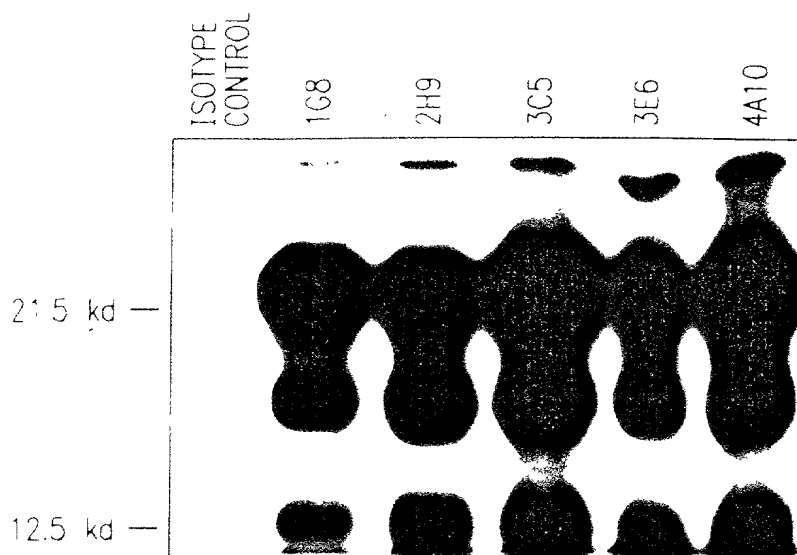


FIG. 37

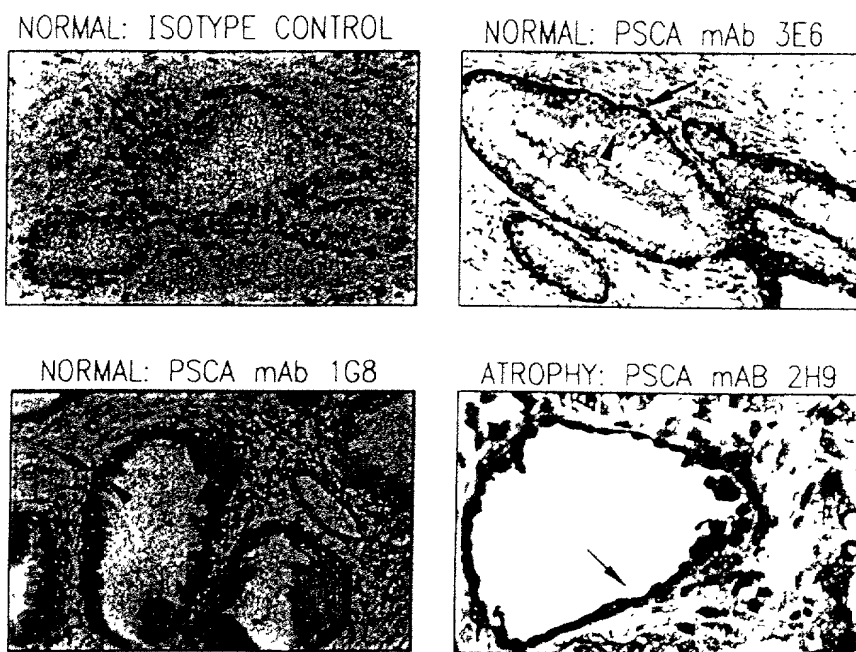
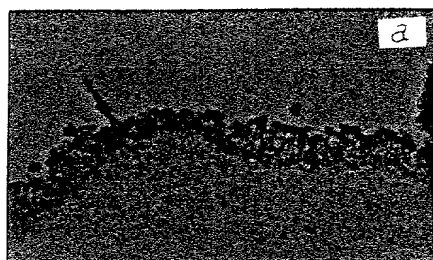
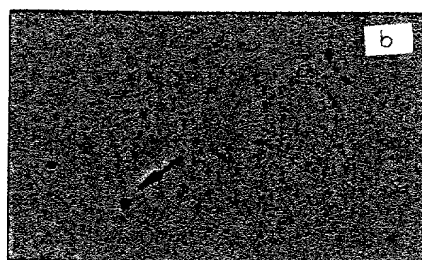


FIG. 38

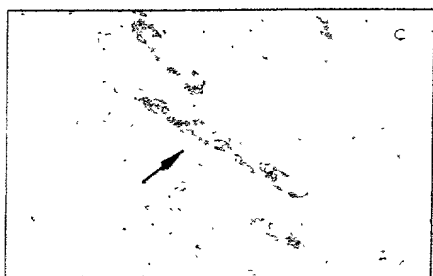
FIG. 39A



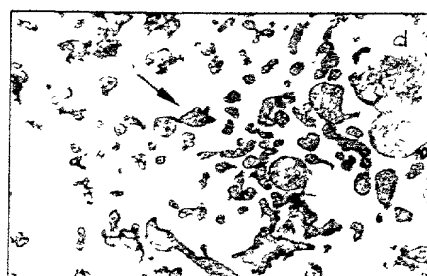
BLADDER: 1G8



COLON: 1G8



KIDNEY: 3E6



PLACENTA: 3E6

PROSTATE

PROSTATE

PROSTATE

KIDNEY

KIDNEY

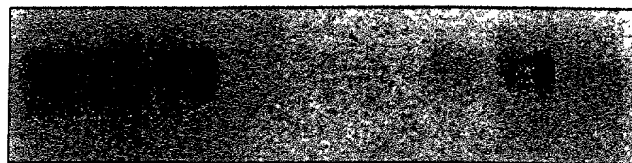
KIDNEY

BLADDER

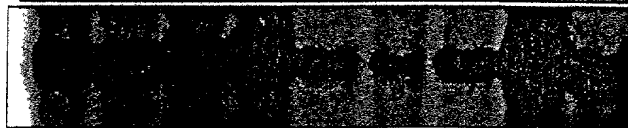
BLADDER

BLADDER

LAPC 9



PSCA



ACTIN

FIG. 39B

005441.030  
T052/0" T845860

FIG. 40A

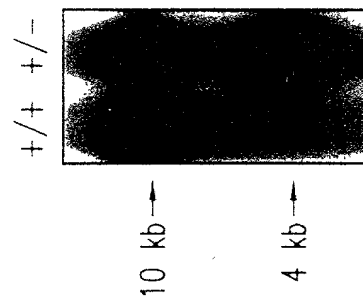
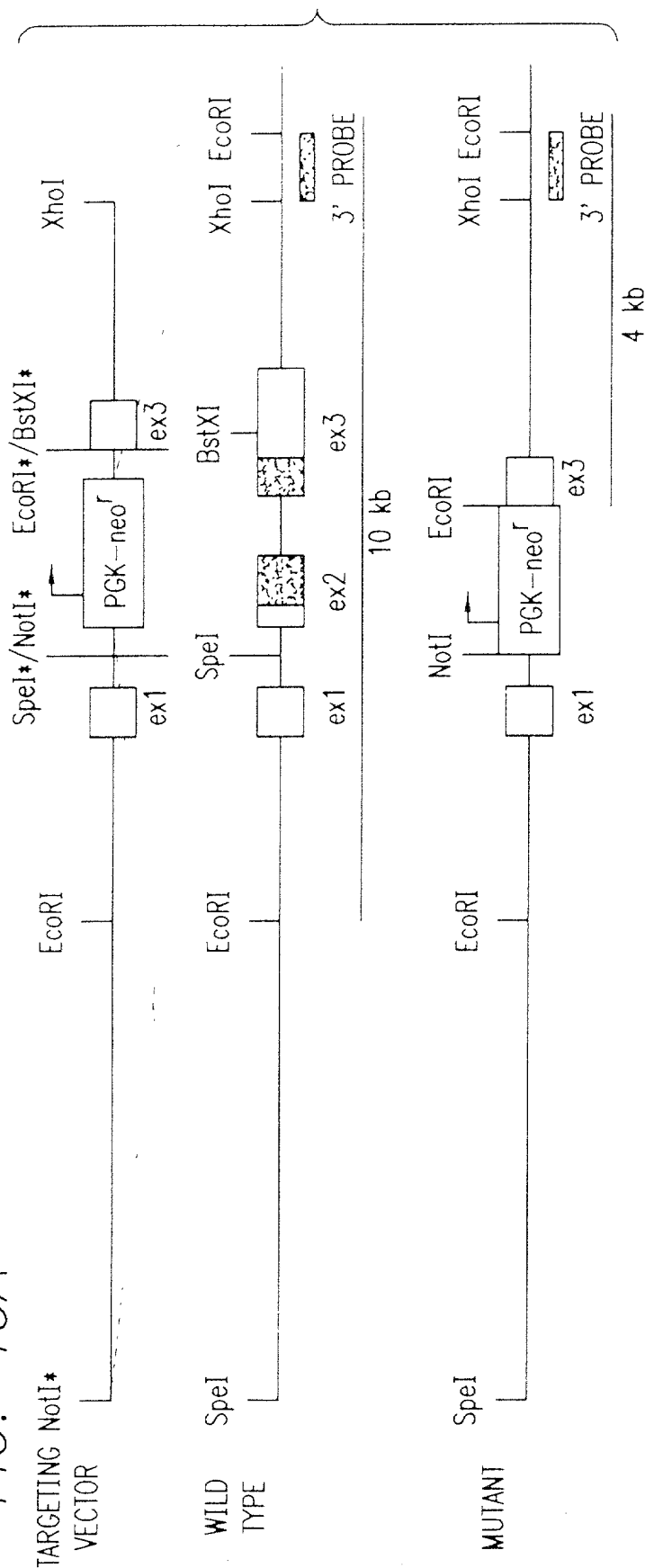
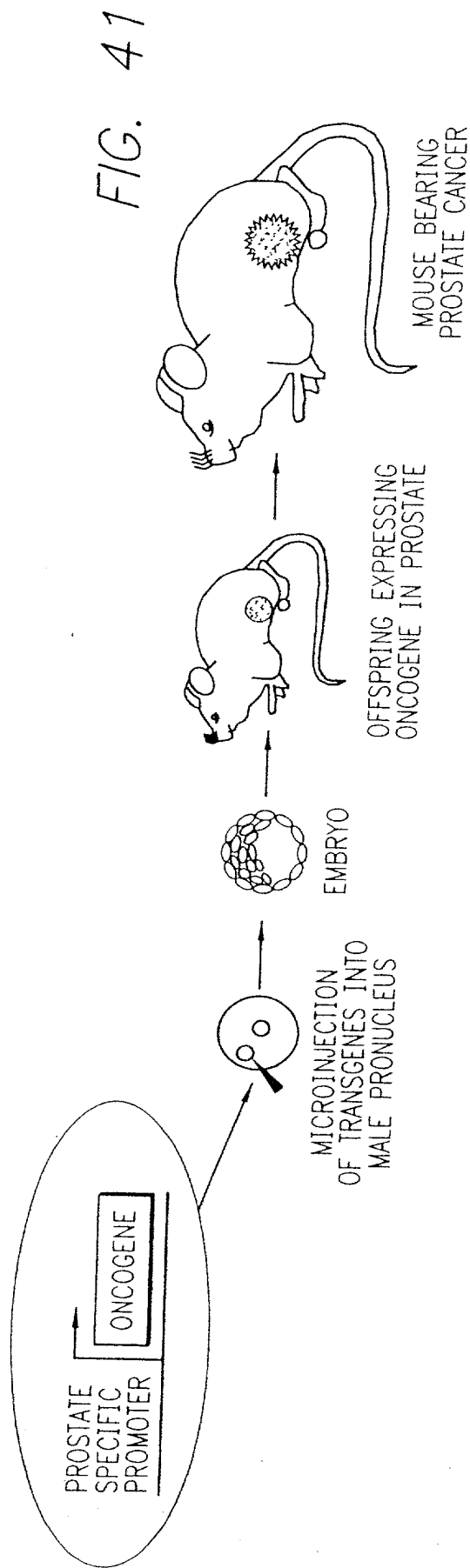


FIG. 40B



TRANSGENE	TARGET TISSUES	CHARACTERISTICS
C3(1) (-3 kb)/ SV40 LARGE+SMALL, T MAROULAKOU et al. 1994 PNAS	PROSTATE (SECRETORY CELLS) URETHRAL, MAMMARY AND SWEAT GLAND	LOW-GRADE PIN 8-12 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 28 WKS NO METASTASES
PROBASIN (-426 bp)/ SV40 LARGE+SMALL, T GREENBERG et al. 1995 PNAS	PROSTATE (SECRETORY CELLS)	LOW-GRADE PIN 5-8 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 12 WKS METASTASES IN LYMPH NODE, LUNG, LIVER AND BONE
CRYPTDIN2 (-6.5 kb)/ SV40 LARGE+SMALL, T GARABEDIAN et al. 1998 PNAS	PROSTATE (NEUROENDOCRINE CELLS) SMALL INTESTINE	LOW-GRADE PIN 8-12 WKS HIGH-GRADE PIN 8-12 WKS INVASIVE CARCINOMA 16 WKS METASTASES IN LYMPH NODE, LUNG, LIVER, AND BONE

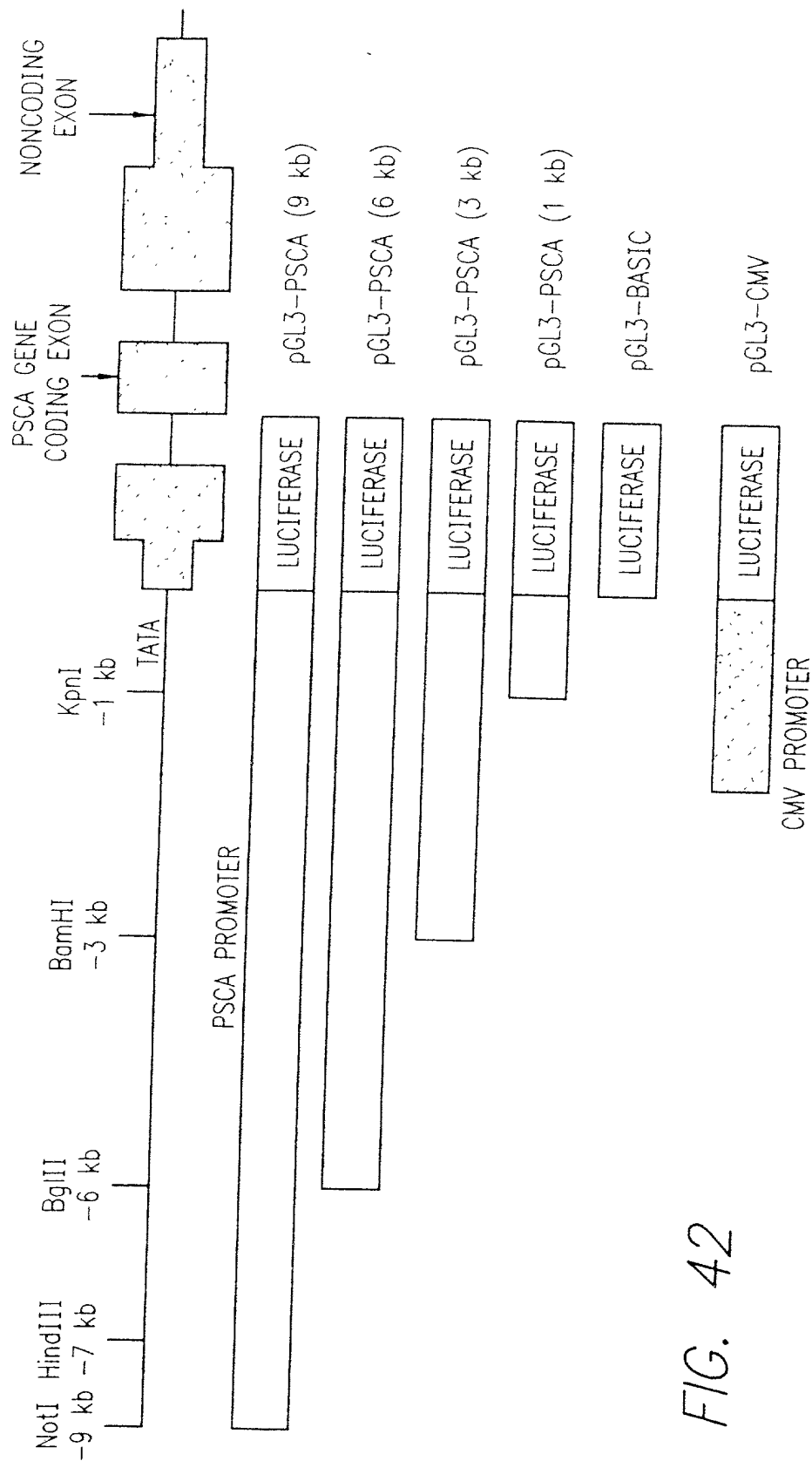


FIG. 42

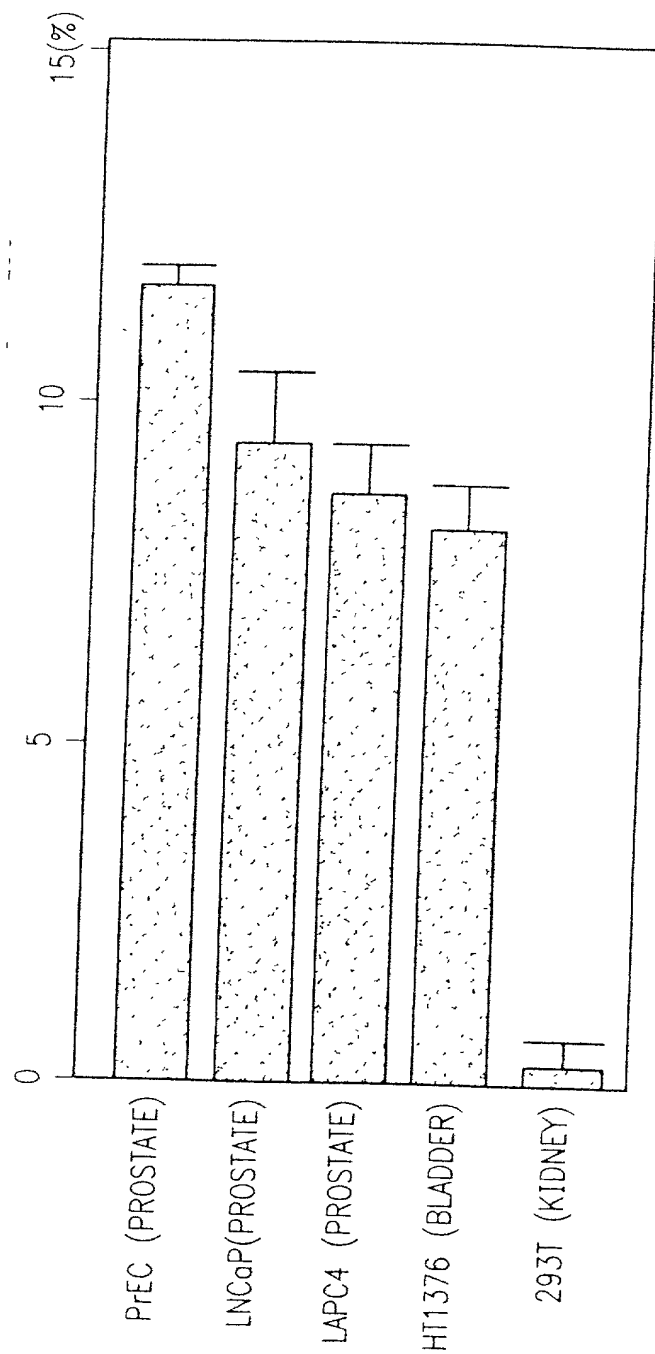


FIG. 43

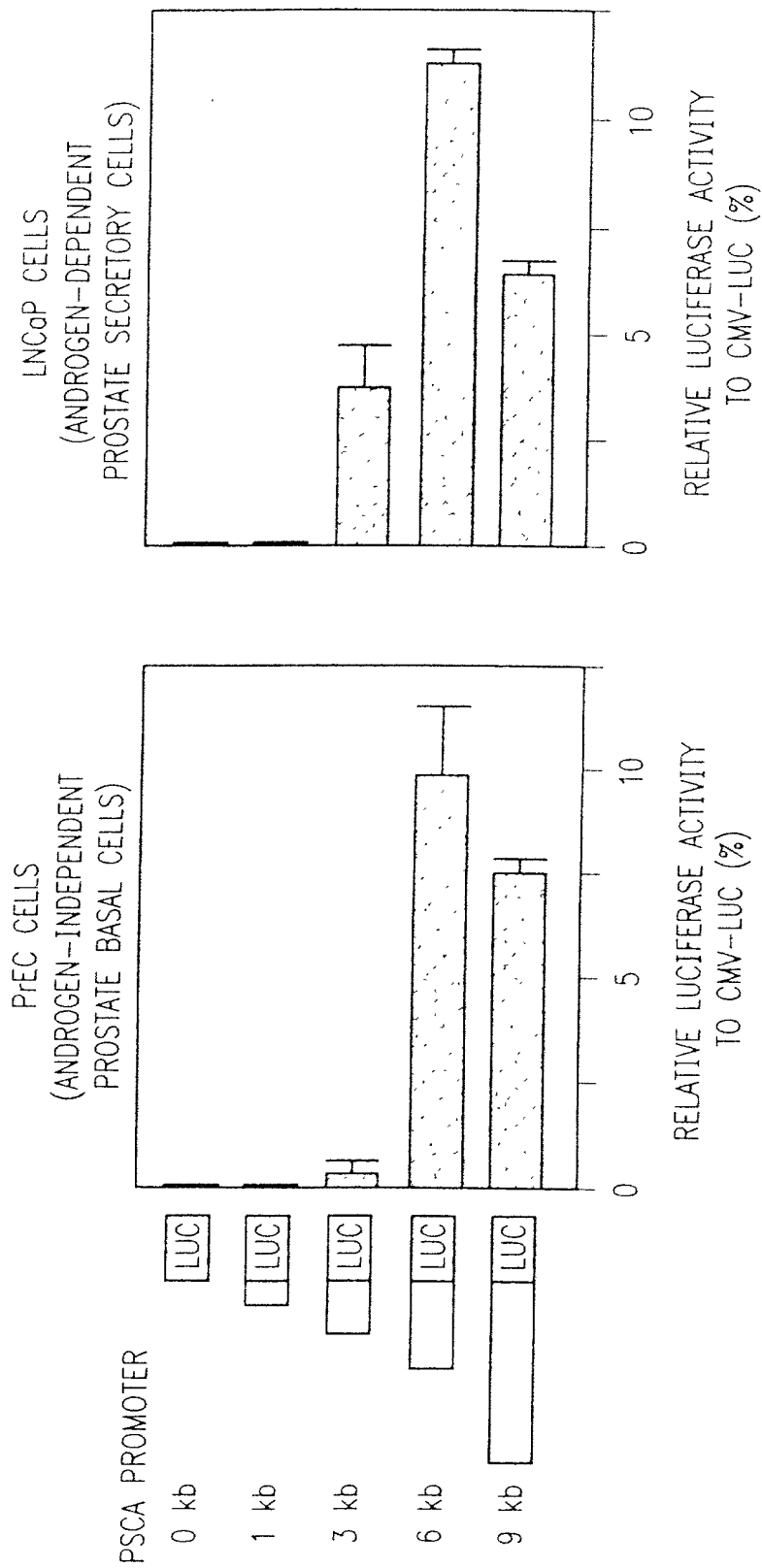
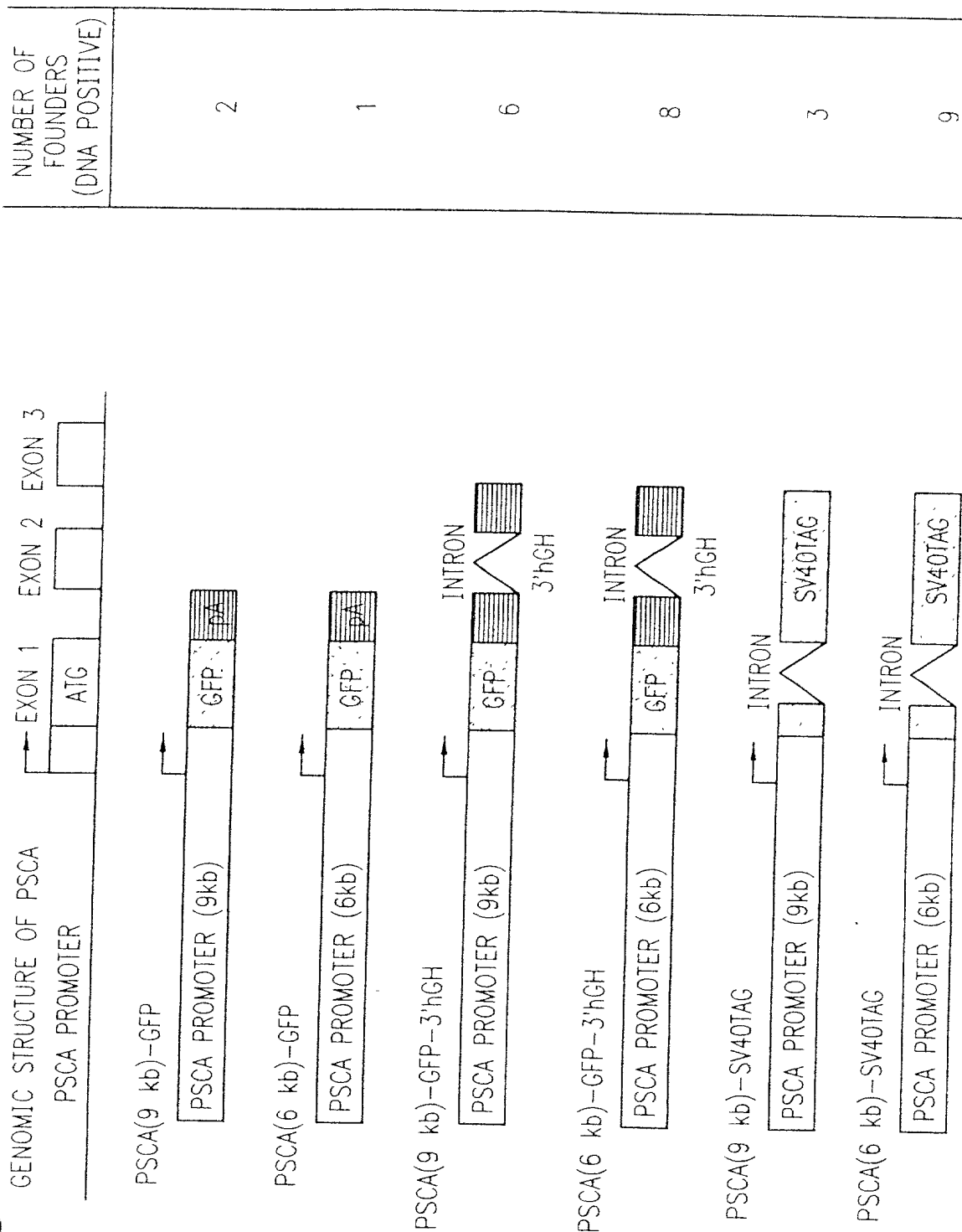


FIG. 44



FIG. 45



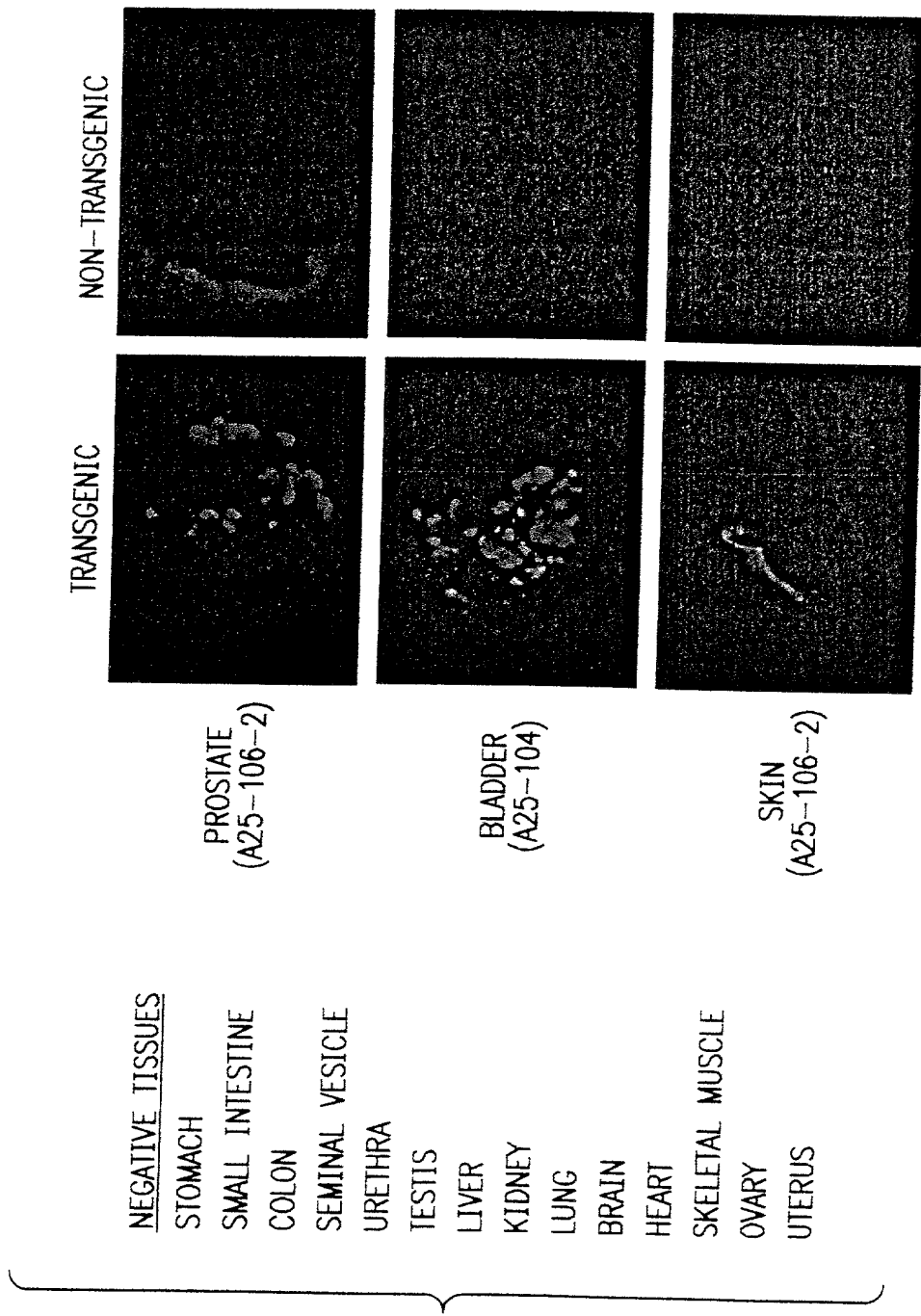


FIG. 46

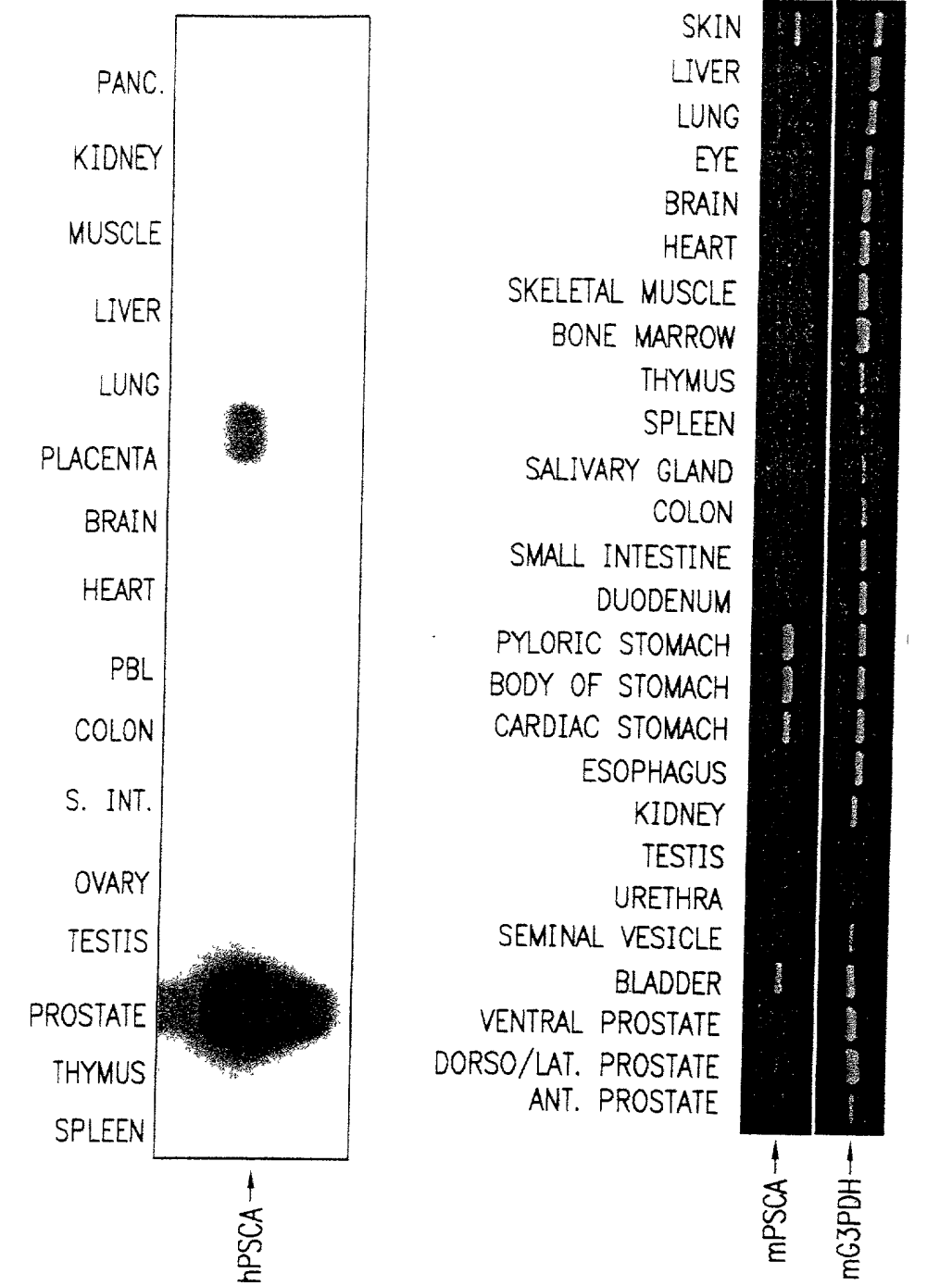


FIG. 47

Table 1. Demographic characteristics of the study population	
<b>Demographic characteristics</b>	
Age (years)	50.0 ± 10.0
Gender	
Male	25 (50%)
Female	25 (50%)
Education level	
High school or less	10 (20%)
University	15 (30%)
Marital status	
Married	15 (30%)
Single	10 (20%)
Divorced	5 (10%)
Widowed	5 (10%)
Occupation	
Unemployed	10 (20%)
Employed	15 (30%)
Retired	5 (10%)
Student	5 (10%)
Health status	
Good	15 (30%)
Fair	10 (20%)
Poor	5 (10%)
Very poor	5 (10%)
Smoking status	
Smoker	10 (20%)
Non-smoker	15 (30%)
Alcohol consumption	
Alcohol consumer	10 (20%)
Non-alcohol consumer	15 (30%)
Family size	
1-2	10 (20%)
3-4	10 (20%)
5-6	5 (10%)
7-8	5 (10%)
9-10	5 (10%)
11-12	5 (10%)
13-14	5 (10%)
15-16	5 (10%)
17-18	5 (10%)
19-20	5 (10%)
21-22	5 (10%)
23-24	5 (10%)
25-26	5 (10%)
27-28	5 (10%)
29-30	5 (10%)
31-32	5 (10%)
33-34	5 (10%)
35-36	5 (10%)
37-38	5 (10%)
39-40	5 (10%)
41-42	5 (10%)
43-44	5 (10%)
45-46	5 (10%)
47-48	5 (10%)
49-50	5 (10%)
51-52	5 (10%)
53-54	5 (10%)
55-56	5 (10%)
57-58	5 (10%)
59-60	5 (10%)
61-62	5 (10%)
63-64	5 (10%)
65-66	5 (10%)
67-68	5 (10%)
69-70	5 (10%)
71-72	5 (10%)
73-74	5 (10%)
75-76	5 (10%)
77-78	5 (10%)
79-80	5 (10%)
81-82	5 (10%)
83-84	5 (10%)
85-86	5 (10%)
87-88	5 (10%)
89-90	5 (10%)
91-92	5 (10%)
93-94	5 (10%)
95-96	5 (10%)
97-98	5 (10%)
99-100	5 (10%)
101-102	5 (10%)
103-104	5 (10%)
105-106	5 (10%)
107-108	5 (10%)
109-110	5 (10%)
111-112	5 (10%)
113-114	5 (10%)
115-116	5 (10%)
117-118	5 (10%)
119-120	5 (10%)
121-122	5 (10%)
123-124	5 (10%)
125-126	5 (10%)
127-128	5 (10%)
129-130	5 (10%)
131-132	5 (10%)
133-134	5 (10%)
135-136	5 (10%)
137-138	5 (10%)
139-140	5 (10%)
141-142	5 (10%)
143-144	5 (10%)
145-146	5 (10%)
147-148	5 (10%)
149-150	5 (10%)
151-152	5 (10%)
153-154	5 (10%)
155-156	5 (10%)
157-158	5 (10%)
159-160	5 (10%)
161-162	5 (10%)
163-164	5 (10%)
165-166	5 (10%)
167-168	5 (10%)
169-170	5 (10%)
171-172	5 (10%)
173-174	5 (10%)
175-176	5 (10%)
177-178	5 (10%)
179-180	5 (10%)
181-182	5 (10%)
183-184	5 (10%)
185-186	5 (10%)
187-188	5 (10%)
189-190	5 (10%)
191-192	5 (10%)
193-194	5 (10%)
195-196	5 (10%)
197-198	5 (10%)
199-200	5 (10%)

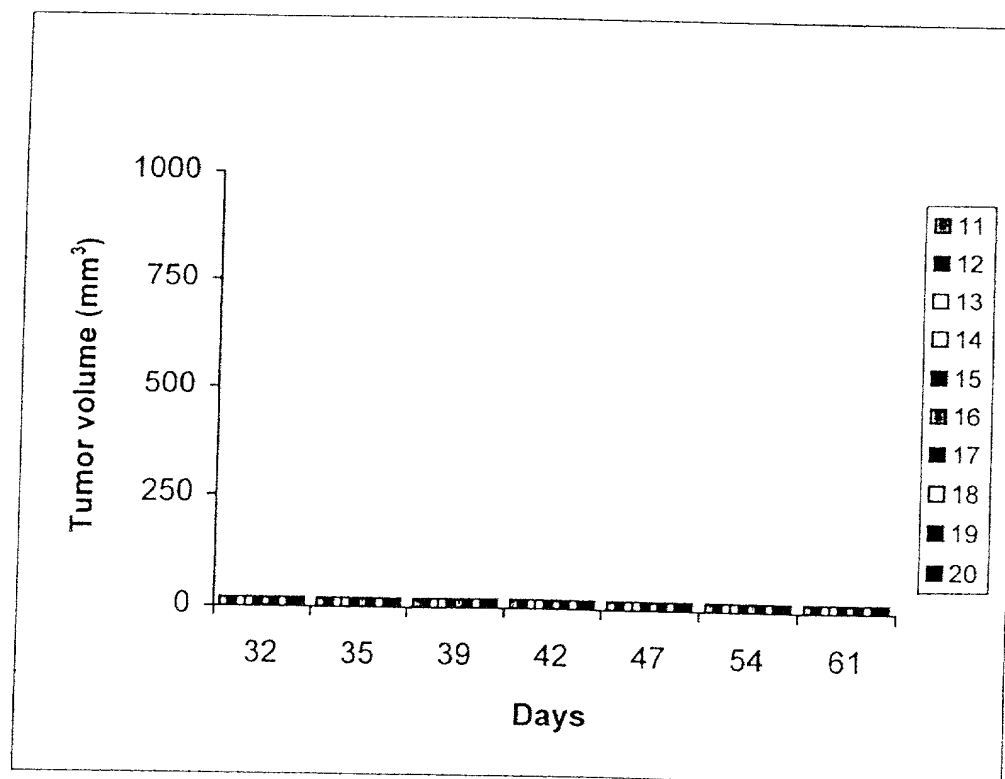
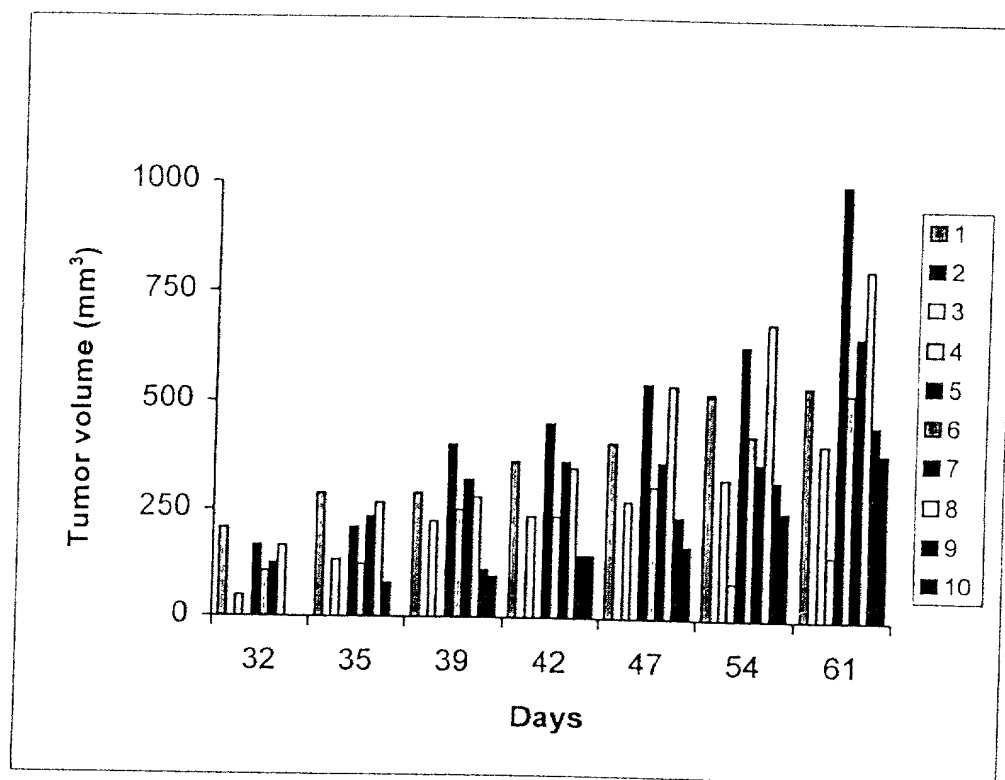


FIG. 49

A

Epitope recognized (OD 450 nm)

<u>mAb</u>	<u>Isotype</u>	<u>F (18-98)</u>	<u>N (2-50)</u>	<u>M (46-109)</u>	<u>C (85-123)</u>
1G8	IgG1 k	1.485	0.004	1.273	0.003
2A2	IgG2a k	0.973	0.631	0.023	0.010
2H9	IgG1 k	1.069	1.026	0.002	0.001
3C5	IgG2a k	1.916	1.709	0.006	0.002
3E6	IgG3 k	1.609	0.036	1.133	2.118
3G3	IgG2a k	2.805	1.731	0.004	0.000
4A10	IgG2a k	1.053	0.493	0.000	0.001

B

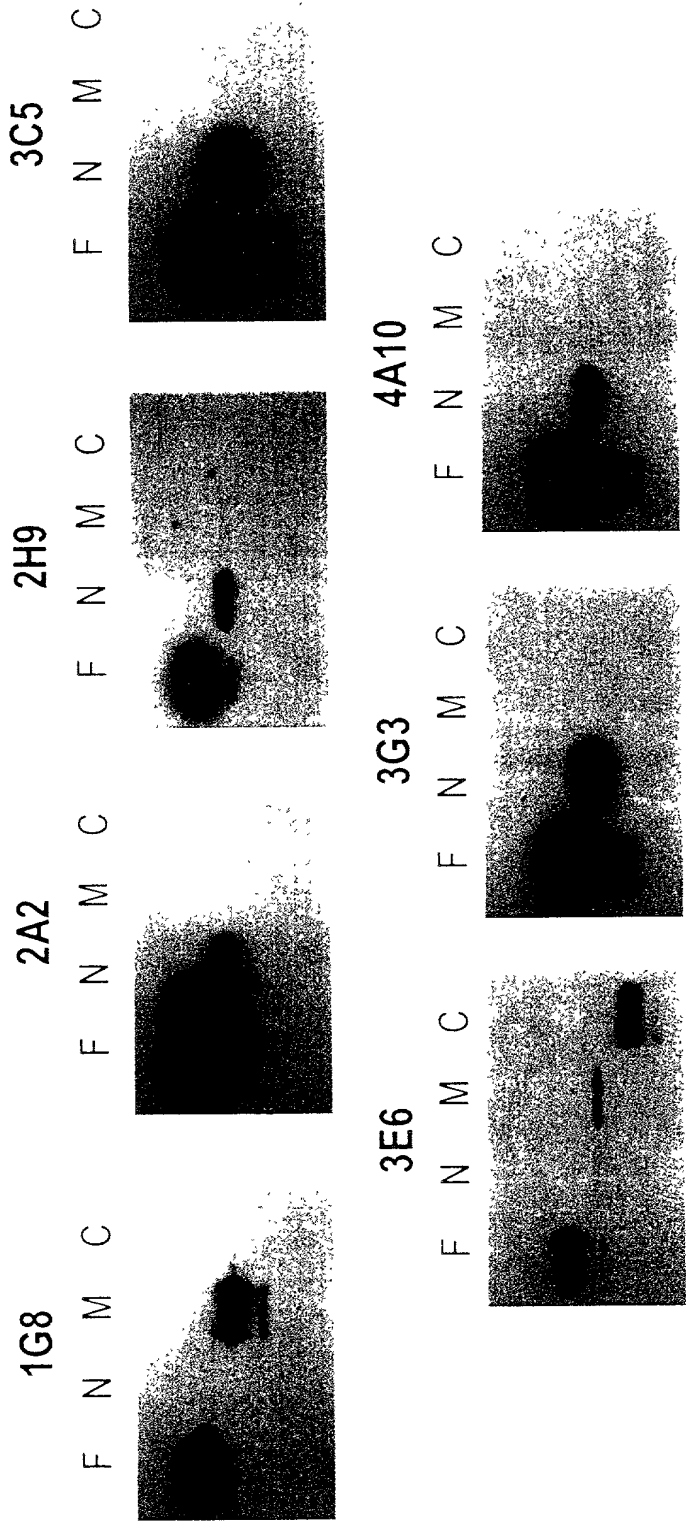
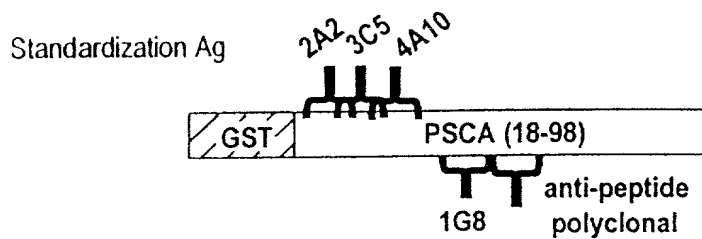
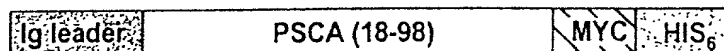


FIG. 50

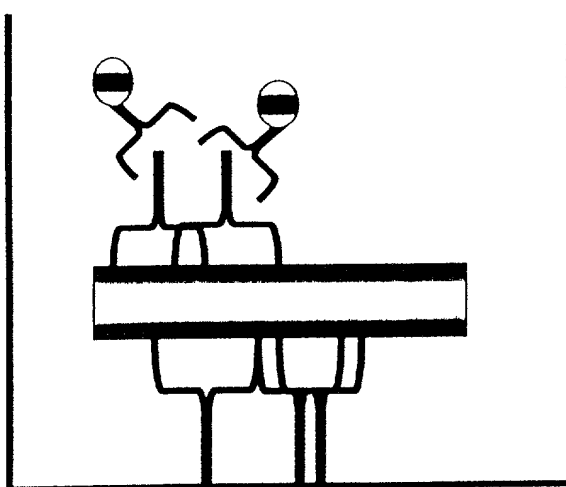
A



Engineered mammalian secreted form



B



Anti-IgG2a HRP

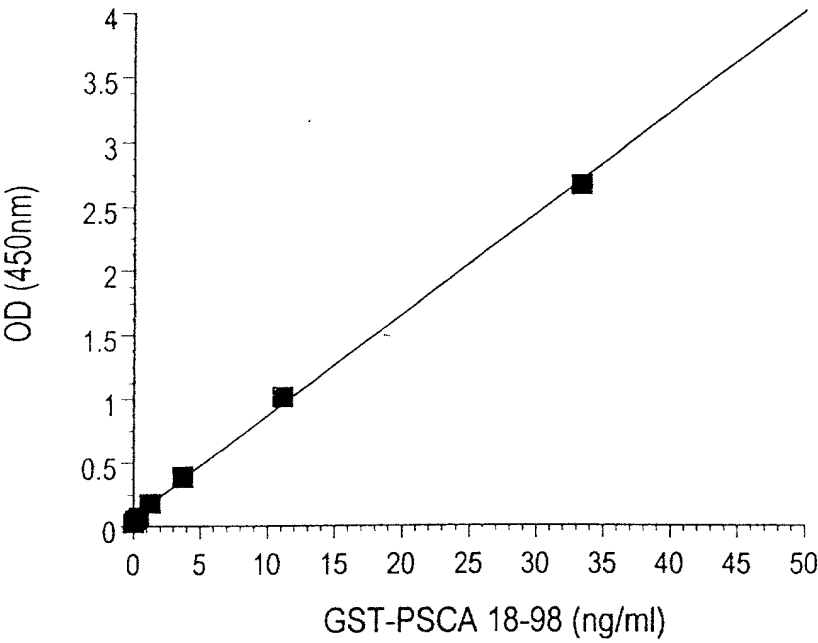
Anti-PSCA mAbs 3C5+4A10+2A2 (IgG2a)

PSCA

Affinity purified anti-peptide polyclonal  
+ mAb 1G8 (IgG1)

FIG. 51

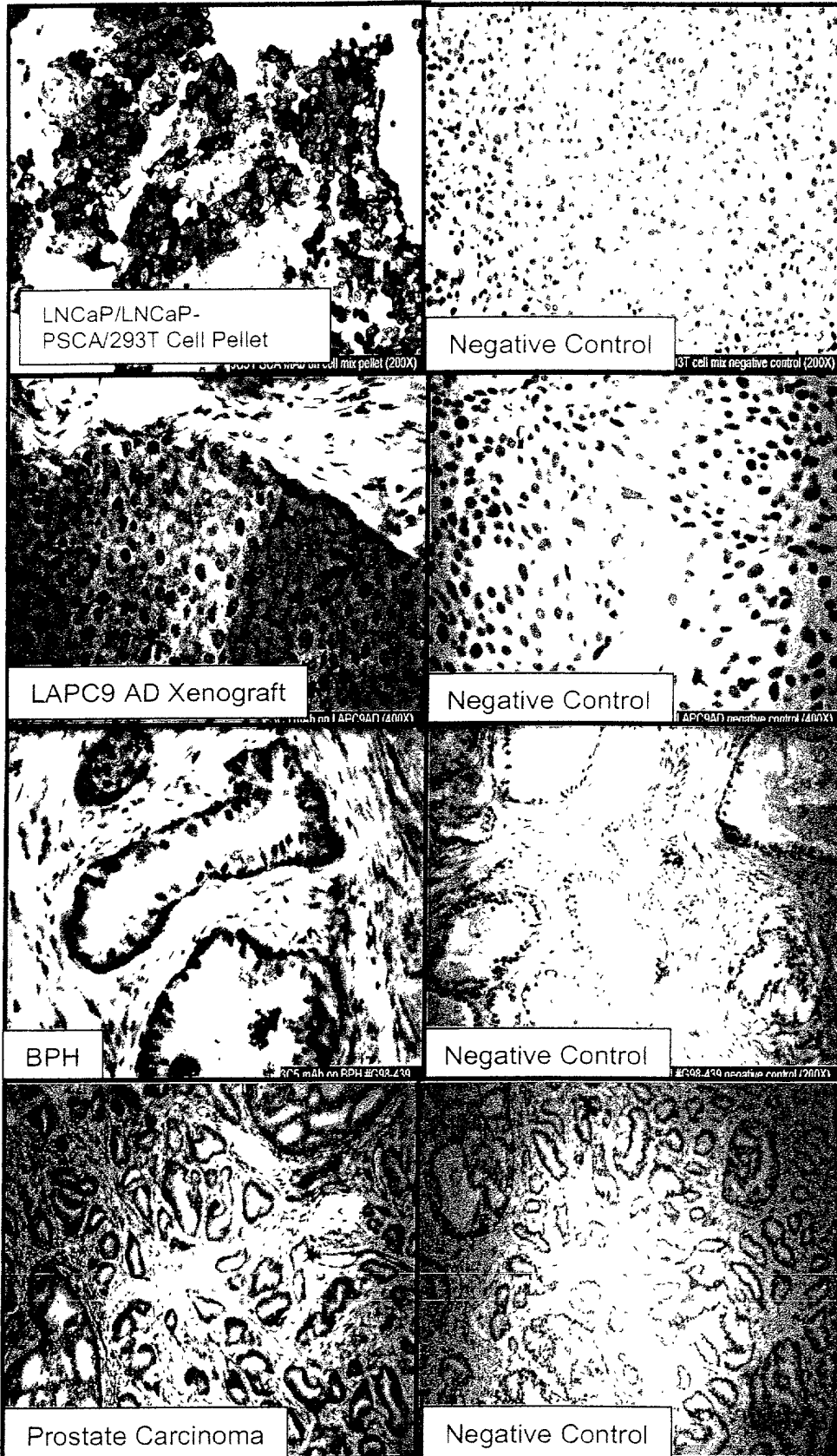
A



B

Sample	OD+range (n=2)	ng/ml
vector	0.005+0.001	ND
vector+hu serum	0.004+0.001	ND
secPSCA	2.695+0.031	32.92
secPSCA+hu serum	2.187+0.029	26.55

FIG. 52



09541-0250



FIG. 53

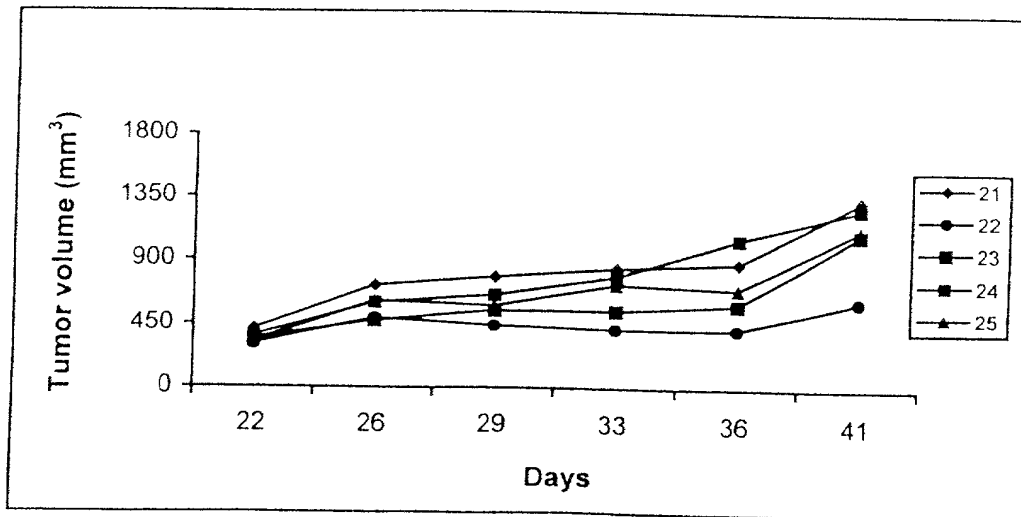
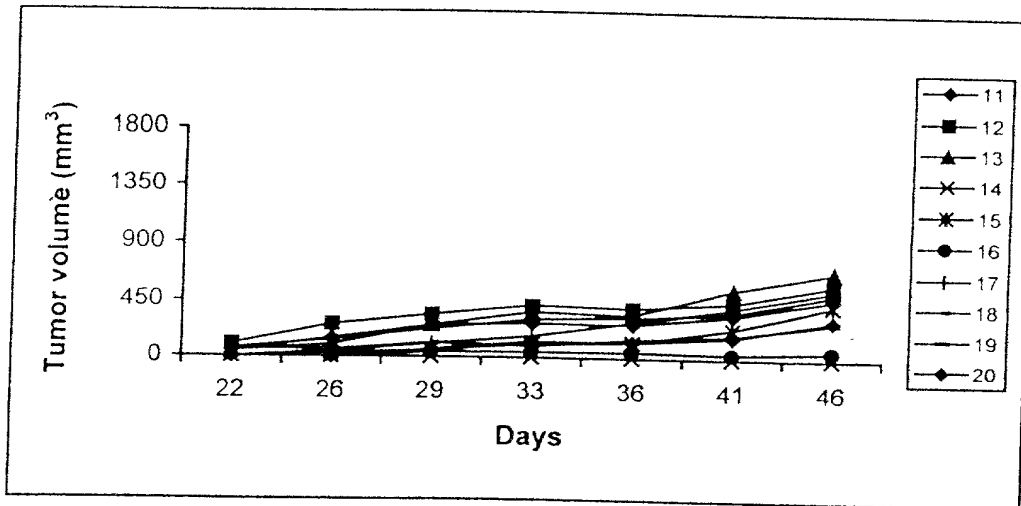
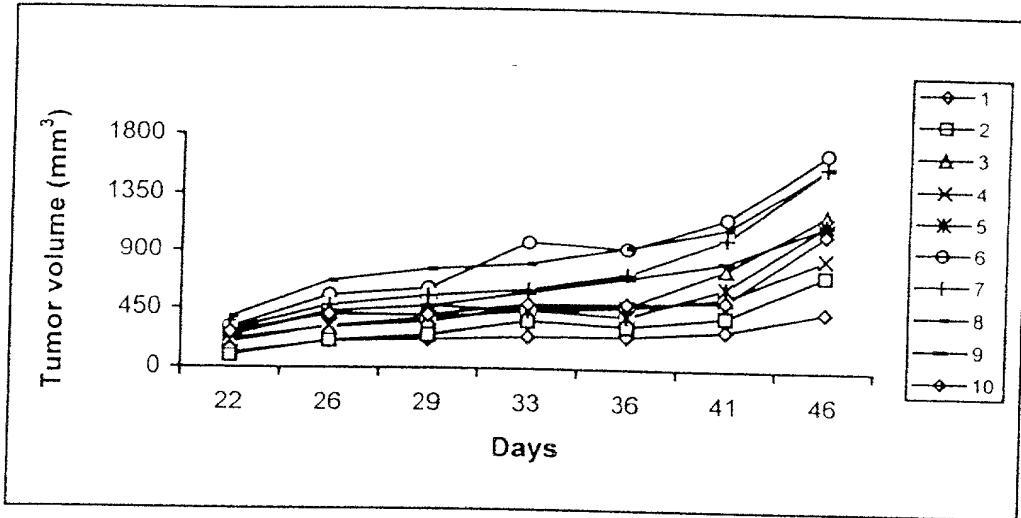


FIG. 54

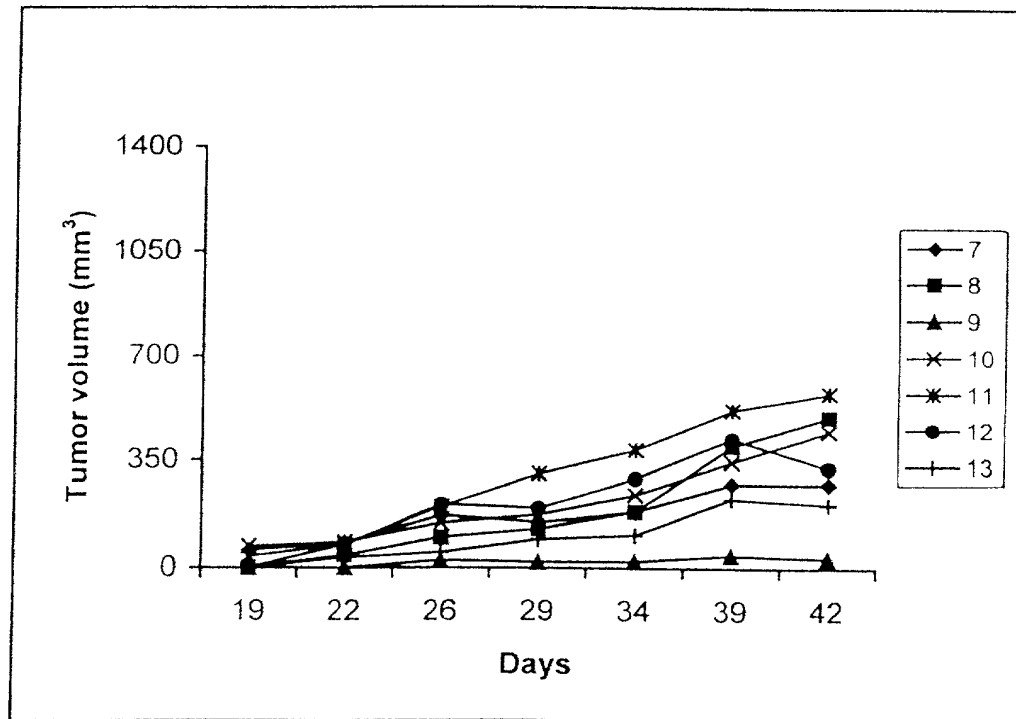
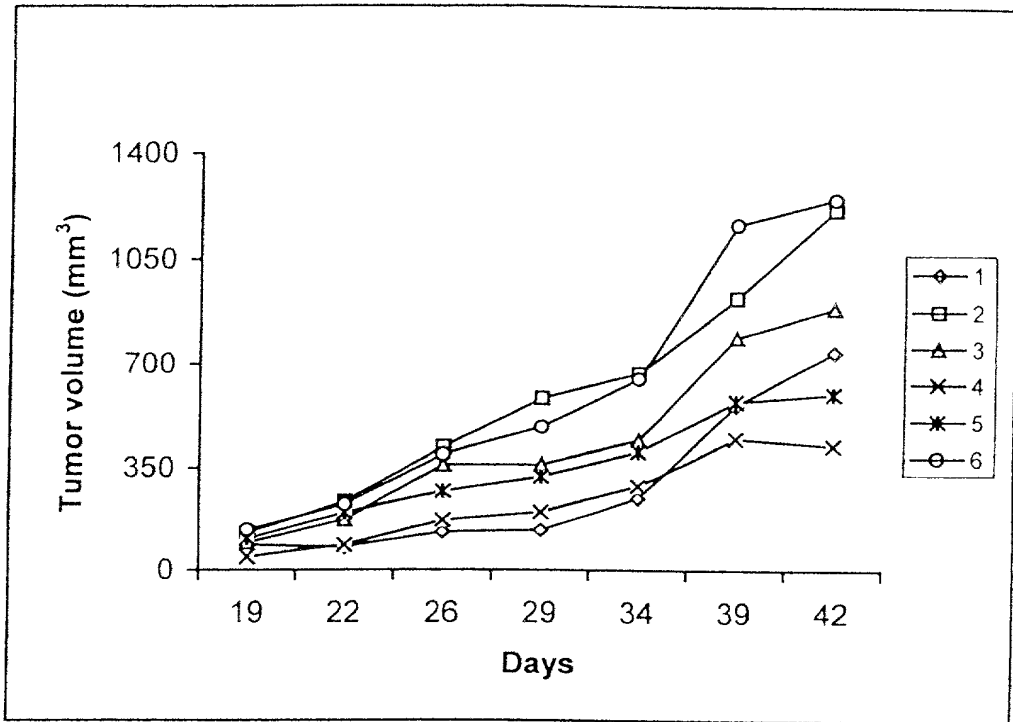


FIG. 55

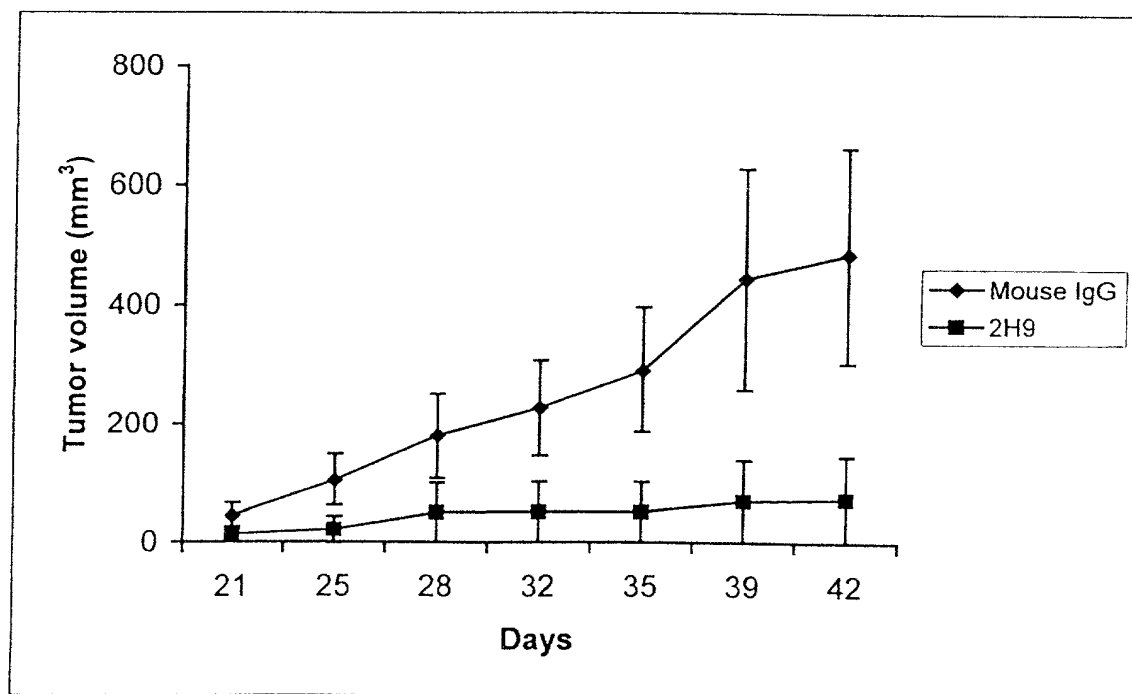
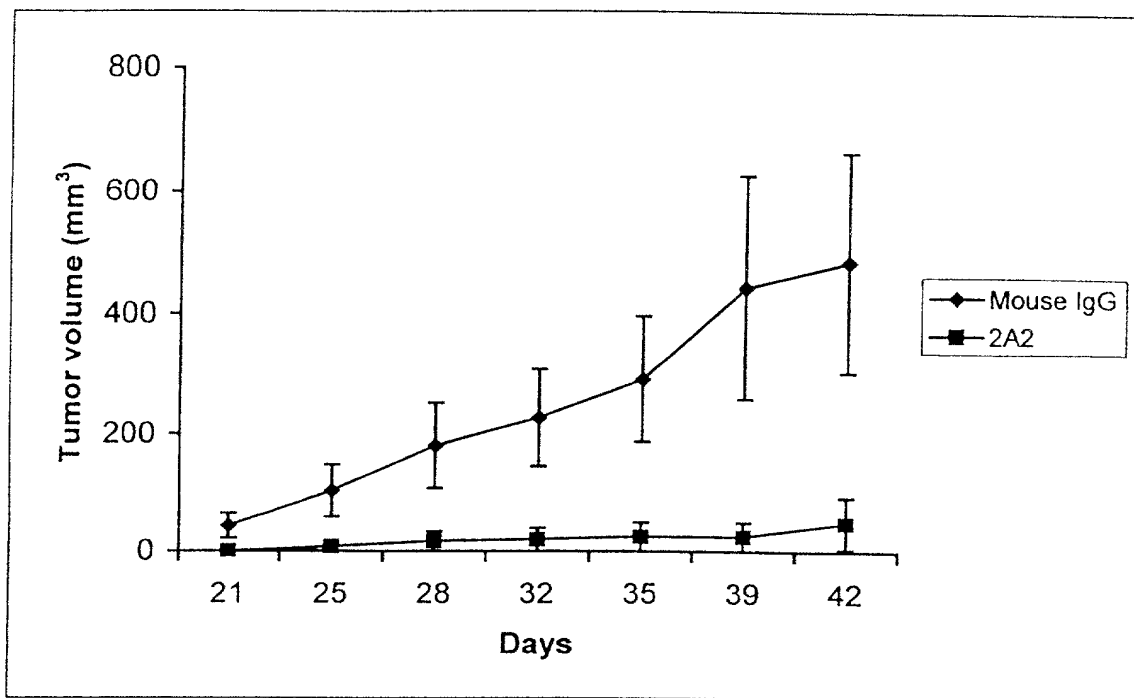


FIG. 56

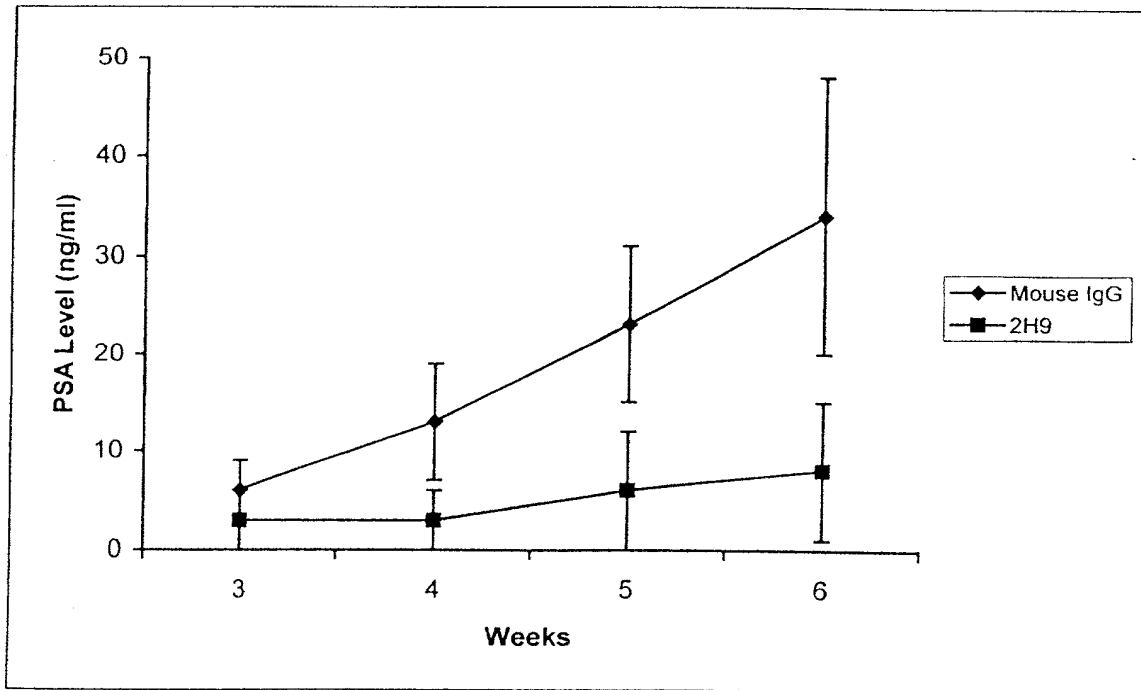
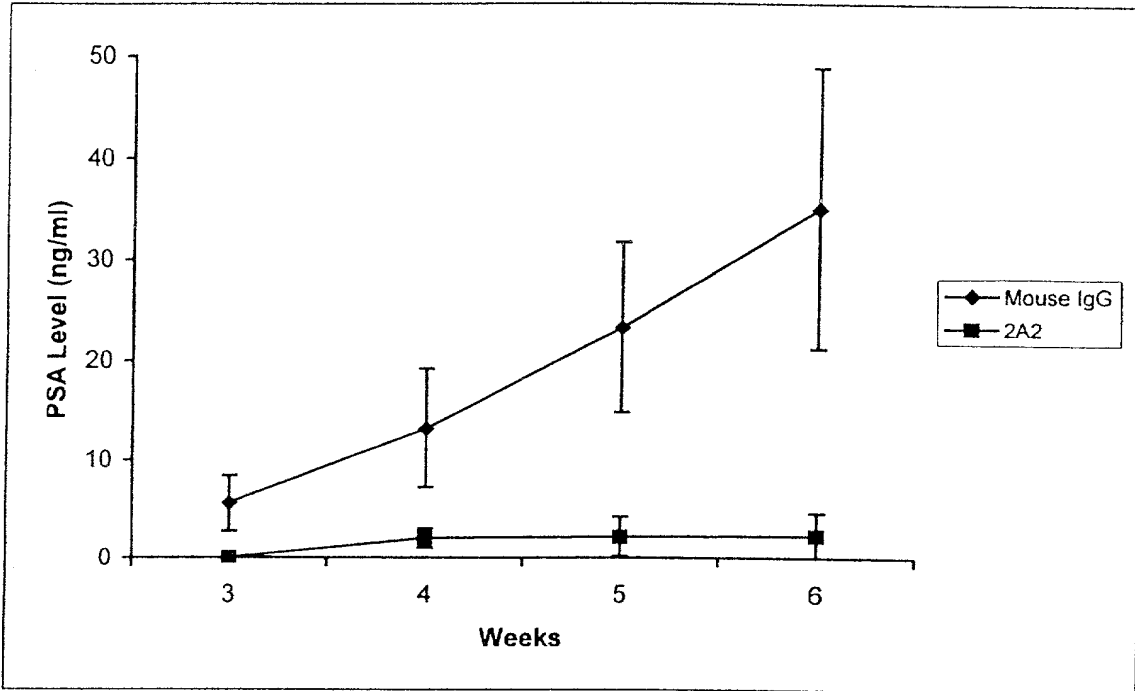


FIG. 57

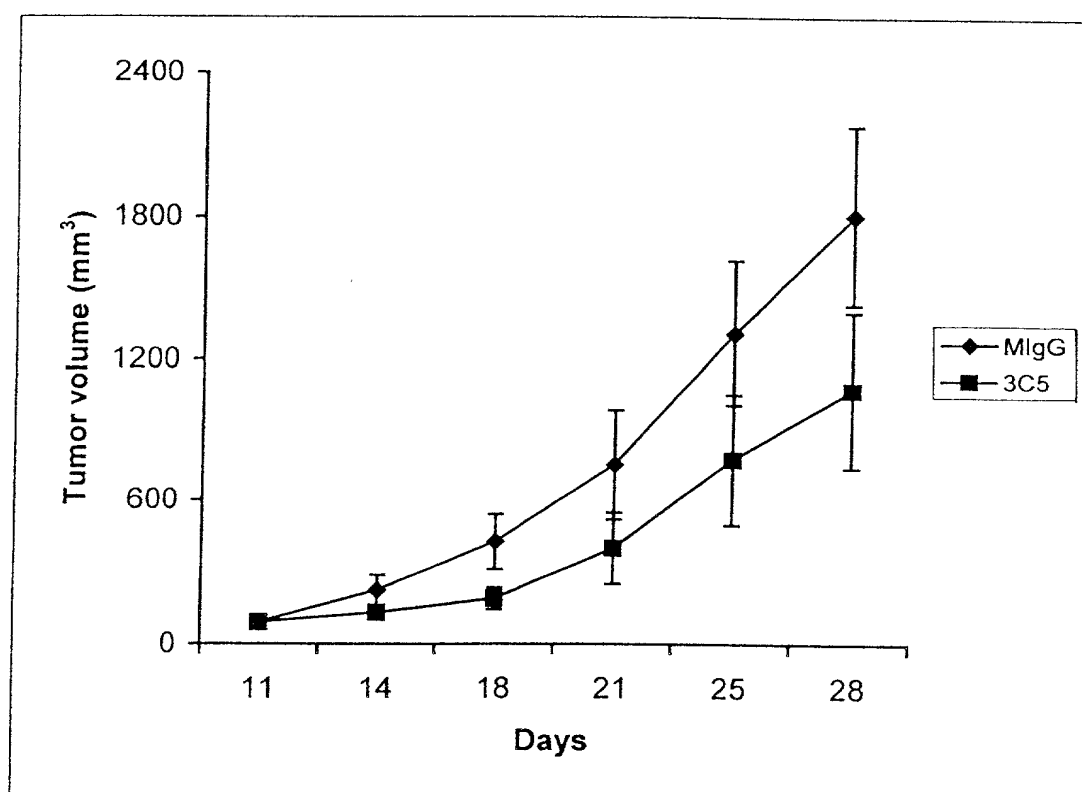


FIG. 58

TGCTTCTTCCTGATGGCAGTGGTTATAGAGTCAATTGAGGTTGAGTGCAGCAGTCT 60  
C F F L M A V V I G V N S E V Q L Q Q S 20

GGGCGAGAACTTGTGAGTCCAGGGCCTCAGTCAAGTTGCTCCTGCACAGCTTCTGGCTTC 120  
G A E L V R S G A S V K L S C T A S G F 40

— CDR1 —  
AACATTAAAGACTACTATATACACTGGGTGAATCAGAGGCCTGACCGGCTGGAGTGG 180  
N I K D Y Y I H W V N Q R P D Q G L E W 60

— CDR2 —  
ATTGGAATGGATTGATCCCTGAGAAATGGTGACACTGAATTTGTCCGAAAGTTCAGGGCAAG 240  
I G W I D P E N G D T E F V P K F Q G K 80

GCCACTATGACTGCAGACATTTTCTCCAACACAGCCTACCTGCACCTCAGCAGCCTGACA 300  
A T M T A D I F S N T A Y L H L S S L T 100

— CDR3 —  
TCTGAAGACACTGCCGTCTATTACTGTAAAACGGGGGTTTCTGGGGCCCAAGGACTCTG 360  
S E D T A V Y Y C K T G G F W G Q G T L 120

GTCACGTCTCTGCAGCCAAACGACACCCCCCATCTGTCTATCCACTG  
V T V S A A K T T P P S V Y P L

FIG. 59

TTGCTAGCAACAGCCTCAGATGTCCACTCCAGGTCCAACTGCAGCAACCTGGGTCTGAA 60  
L V A T A S D V H S Q V Q L Q Q P G S E 20

CTGCTGAGGCCCTGGAACTTCAGTGAAGCTGTCTCTGCAAGGCTTCTGGCTATACATTCTCC 120  
L V R P G T S V K L S C K A S G Y T F S 40  
CDR1

AGCTACTGGATGCACTGGGTGAAGCAGAGGCCCTGGACAAGCCTTGAGTGGATTGGAAT 180  
S Y W M H W V K Q R P G Q G L E W I G N 60

ATTGACCCTGGTAGTGGTTACACTAACTACGCTGAGAACCTCAAGACCAAGGCCACACTG 240  
I D P G S G Y T N Y A E N L K T K A T L 80  
CDR2

ACTGTAGACACATCCTCCAGCACAGCCCTACATGCAGCTCAGCAGCCTGACATCTGAGGAC 300  
T V D T S S S T A Y M Q L S S L T S E D 100

TCTGCAGTCTATTACTGTACAAGCCGATCTACTATGATTACGACGGGATTTGCTTACTGG 360  
S A V Y Y C T S R S T M I T T G F A Y W 120  
CDR3

GGCCAAGGACTCTGGTCACTGTCTCTGCAGCTACAACAAGCCCATCTGTCTATCCA 420  
G Q G T L V T V S A A T T T A P S V Y P 160

CTGGCC  
L A

FIG. 60

AATGACTTCGGGTTGAGCTGGGTTTTATTATTGTTCTTTTAAAGGGTCCGGAGTGAA 60  
N D F G L S W V F I I V L L K G V R S E 20

GTGAGCCTTGAGGAGTCTGGAGGAGGCTGGGTGCAACCTGGAGGATCCATGAAACTCTCC 120  
V R L E E S G G G W V Q P G G S M K L S 40

TGTGTAGCCTCTGGATTACTTTCAGTAATTACTGGATGACTTGGGTCGCCAGTCTCCA 180  
C V A S G F T F S N Y W M T W V R Q S P 60  
CDR1

GAGAAGGGCTTGAGTGGGTTGCTGAAATTCGATTGAGATCTGAAAATTATGCAACACAT 240  
E K G L E W V A E I R L R S E N Y A T H 80  
CDR2

TATGCGGAGTCTGTGAAAGGAAATTCACCATCTCAAGAGATGATTCAGAAAGTCGTCTC 300  
Y A E S V K G K F T I S R D D S R S R L 100

TACCTGCAATGAACAACCTTAAGACCTGAAGACAGTGAATTTATTACTGTACAGATGGT 360  
Y L Q M N N L R P E D S G I Y Y C T D G 120

CTGGGACGACCTAACTGGGGCCAGGGACTCTGGTCACTGTCTCTGCGAGCCAAACGACA 420  
L G R P N W G Q G T L V T V S A A K T T 140  
CDR3

CCCCCATCTGTCTATCCACTGGCCCCCTTGTGTA  
P P S V Y P L A P C V



FIG. 61

CDR1 Comparisons

1G8	1gG <sub>1k</sub>	Middle	G	F	N	I	K	D	Y	Y	I	H
2H9	1gG <sub>1k</sub>	N-Term.	G	F	T	F	S	N	Y	W	M	T
4A10	1gG <sub>2ak</sub>	N-Term.	G	Y	T	F	S	S	Y	W	M	H

CDR2 Comparisons

1G8	1gG <sub>1k</sub>	W	I	D	P	E	N	G	D	T	E	F	V	P	K	F	Q	G		
2H9	1gG <sub>1k</sub>	E	I	R	L	R	S	E	N	Y	A	T	H	Y	A	E	S	V	K	G
4A10	1gG <sub>2ak</sub>	N	I	D	P	G	S	G	Y	T	N	Y	A	E	N	L	K	T		

CDR3 Comparisons

1G8	1gG <sub>1k</sub>	G	G	F																
2H9	1gG <sub>1k</sub>	L	G	R	P	N														
4A10	1gG <sub>2ak</sub>	R	S	T	M	I	T	T	G	F	A	Y								

09854811.072501

FIG. 62

A



B



C



D



FIG. 63

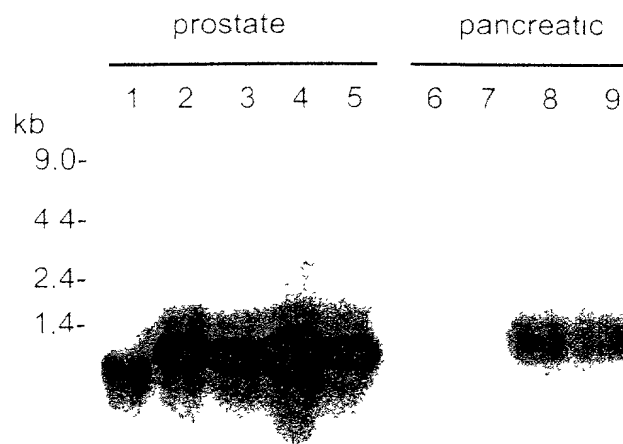


FIG. 64

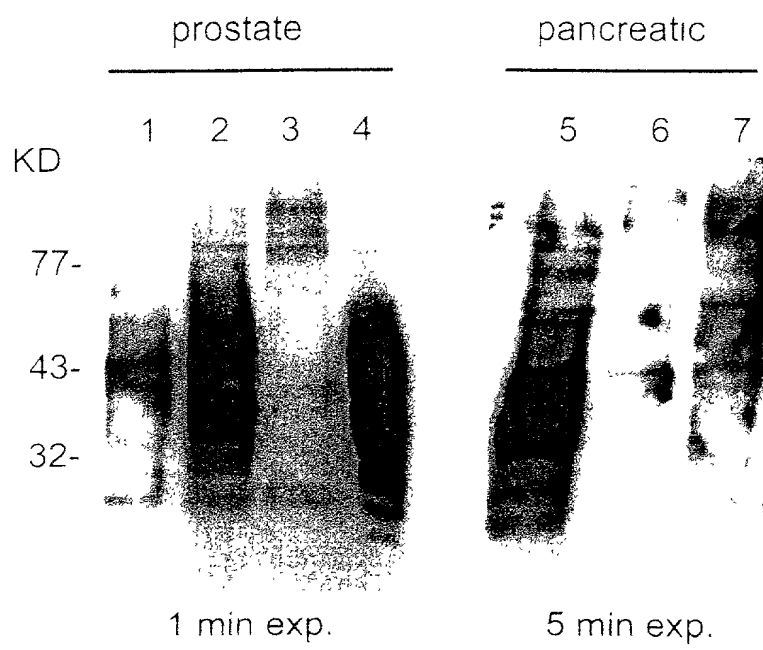


FIG. 65

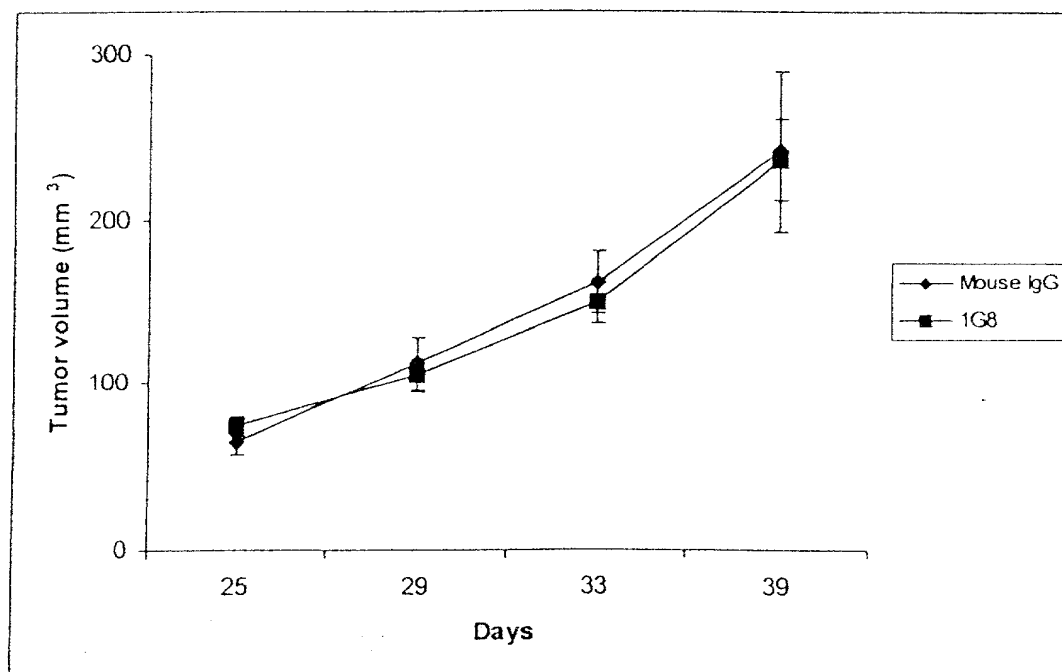
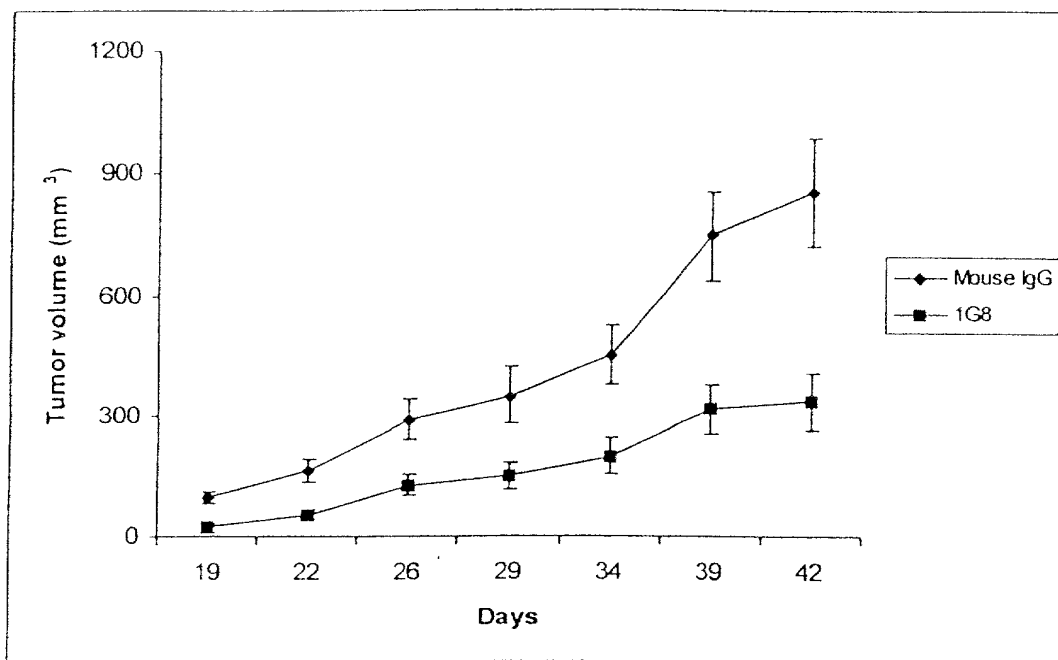
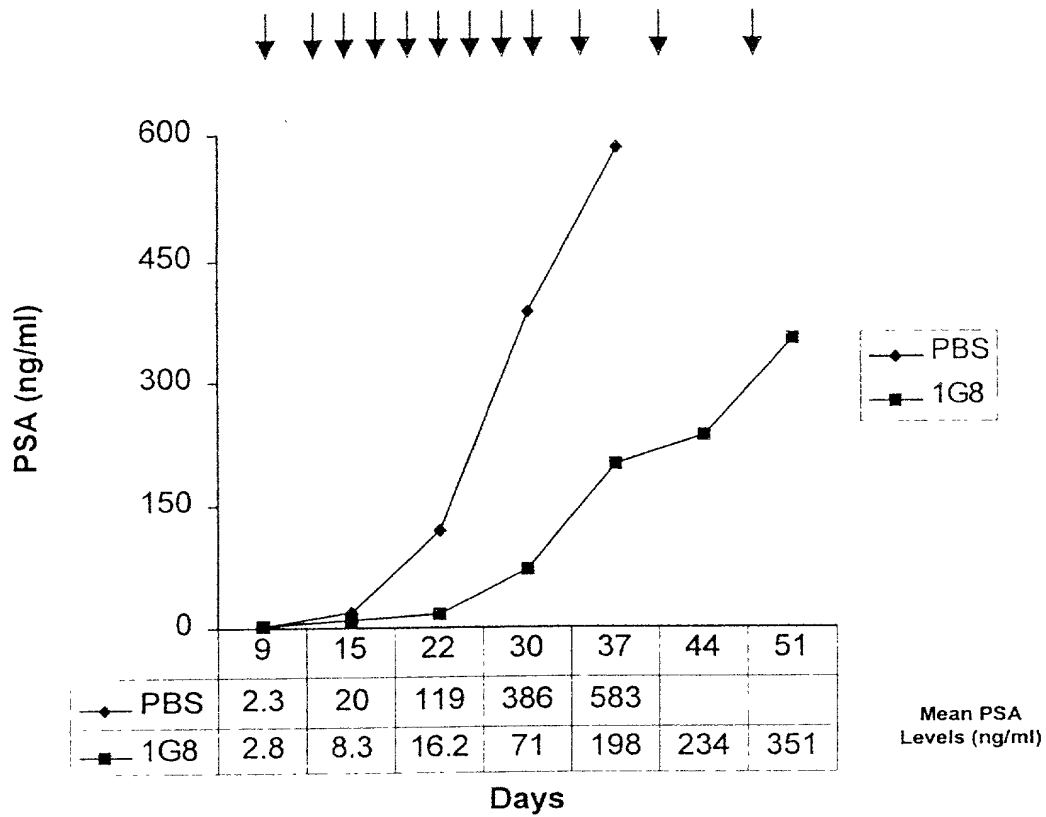


FIG. 66

A)



B)

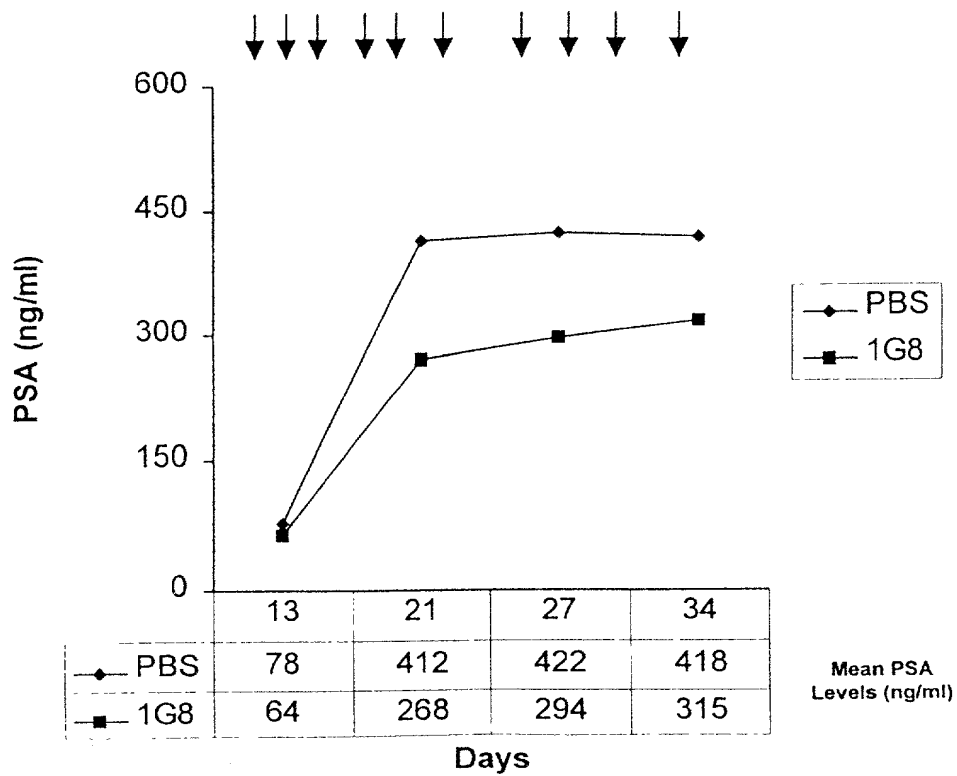
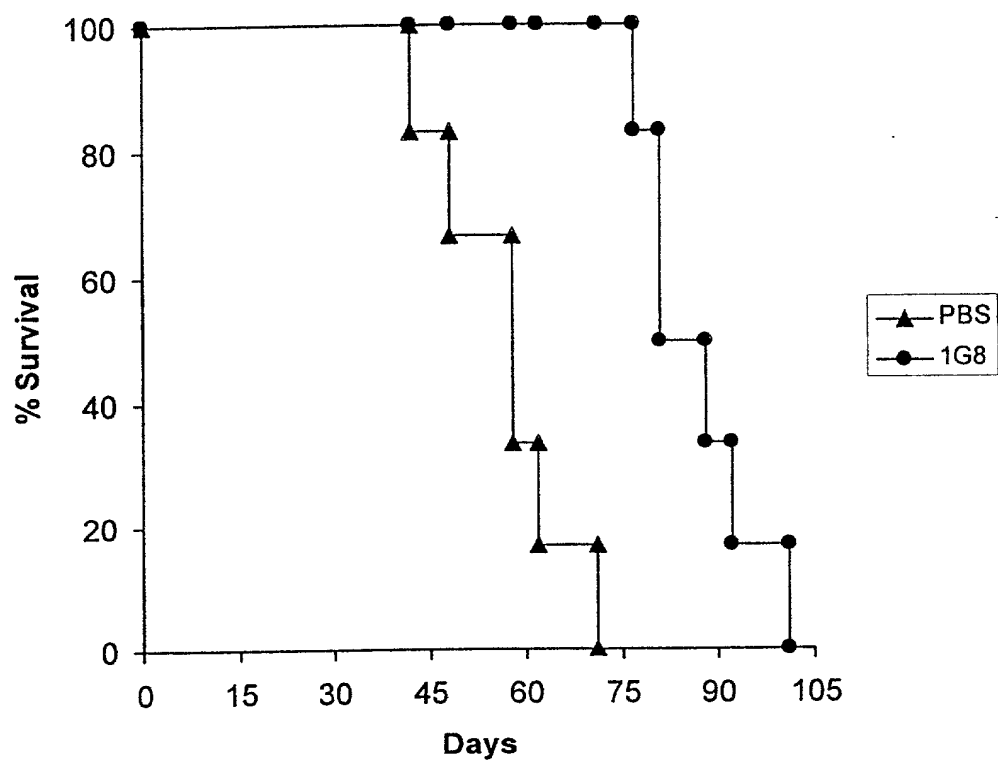
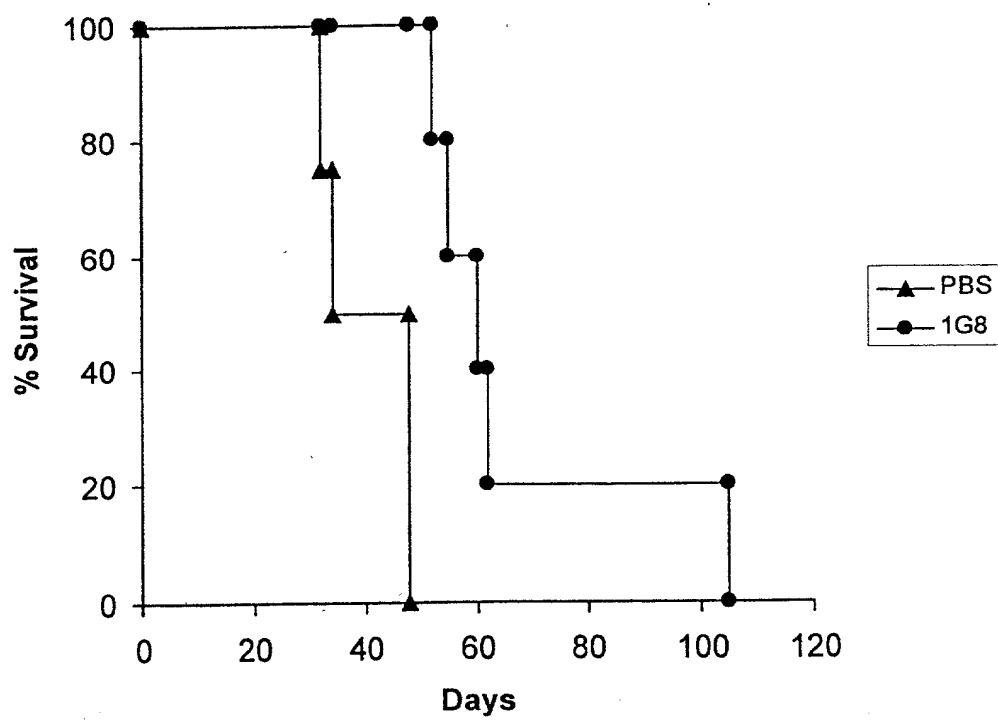


FIG. 67

A)

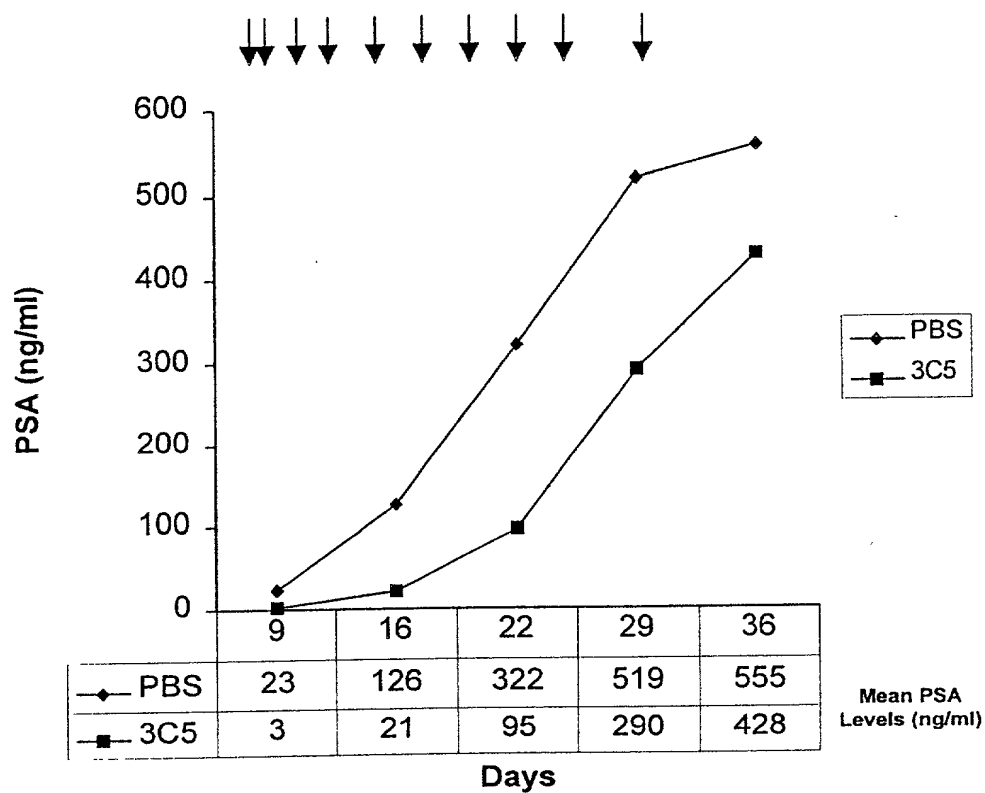


B)



# FIG. 68

A)



B)

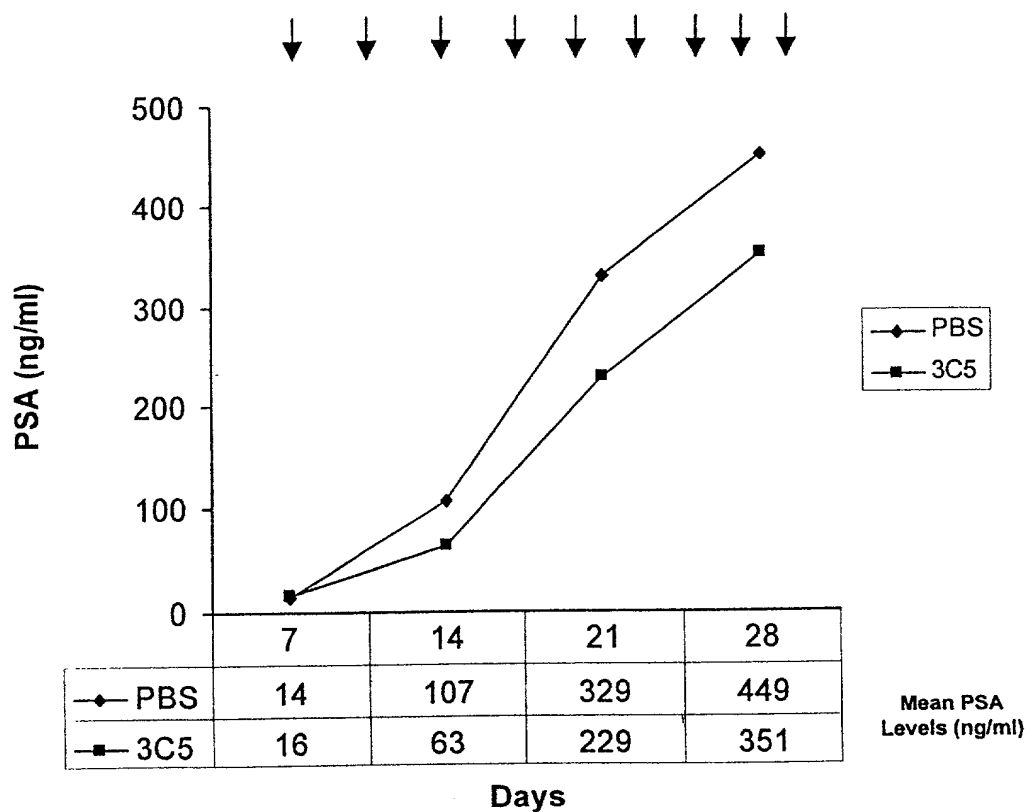
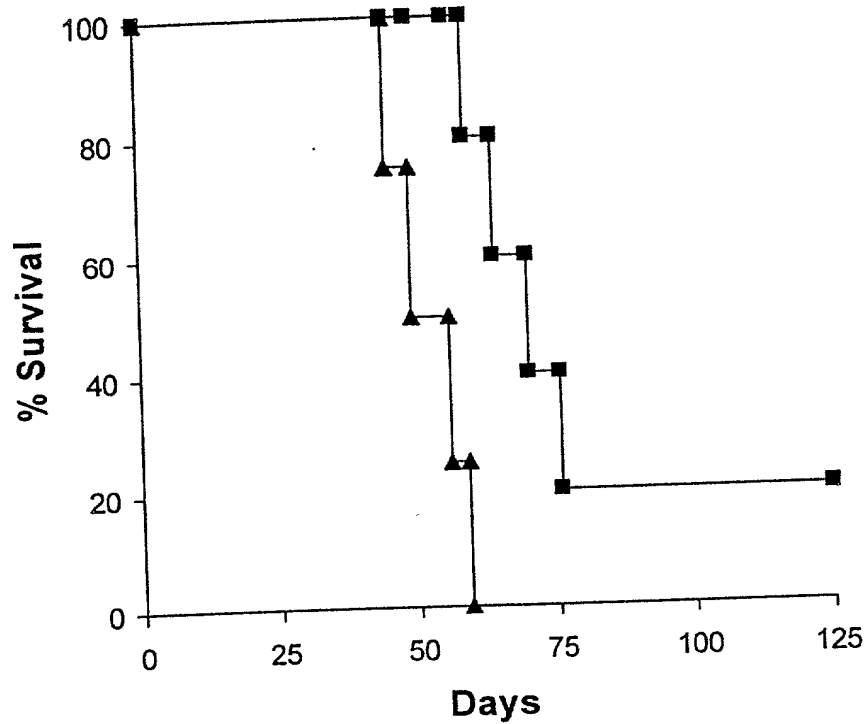




FIG. 69

A)



B)

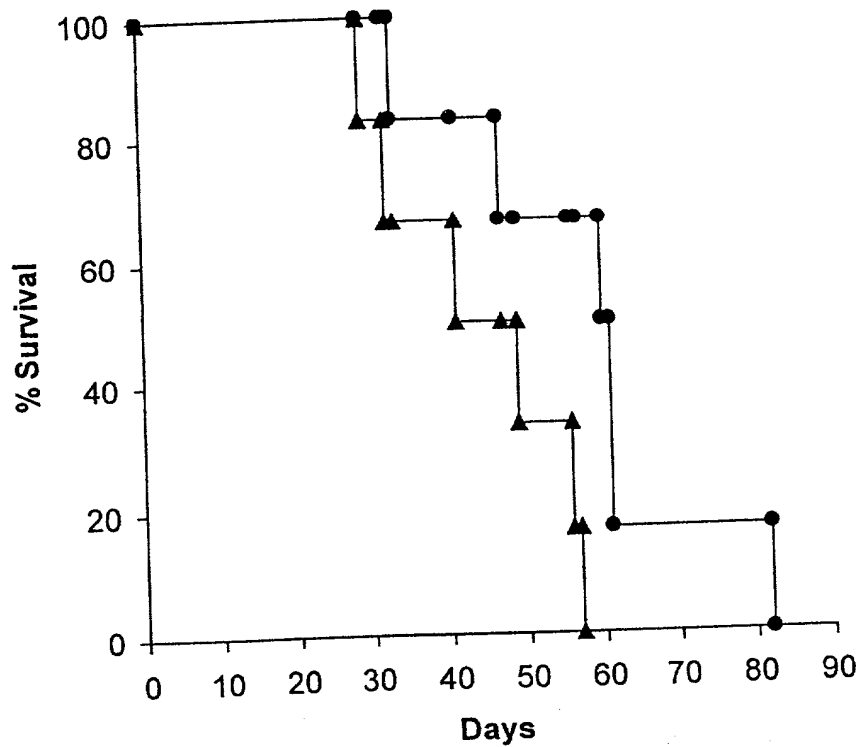
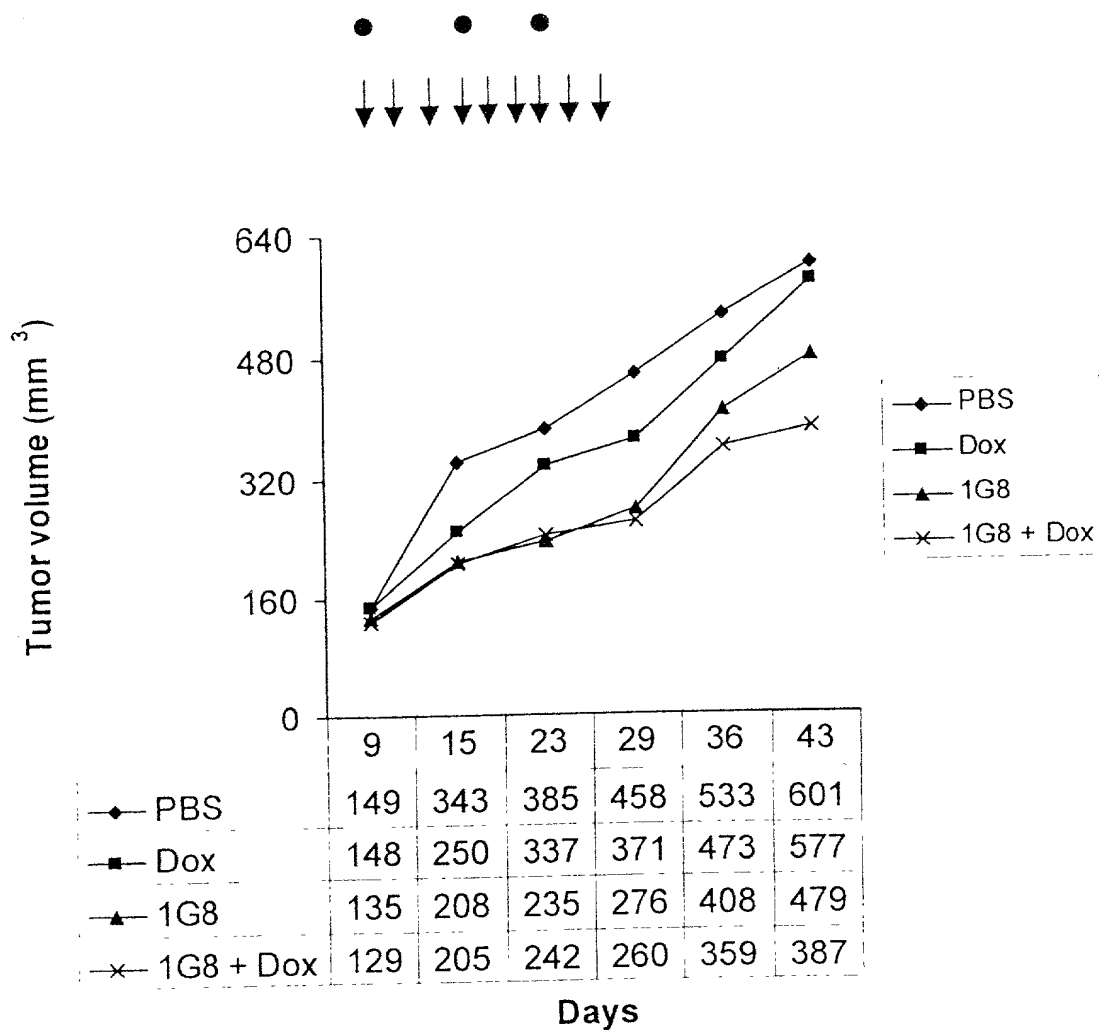


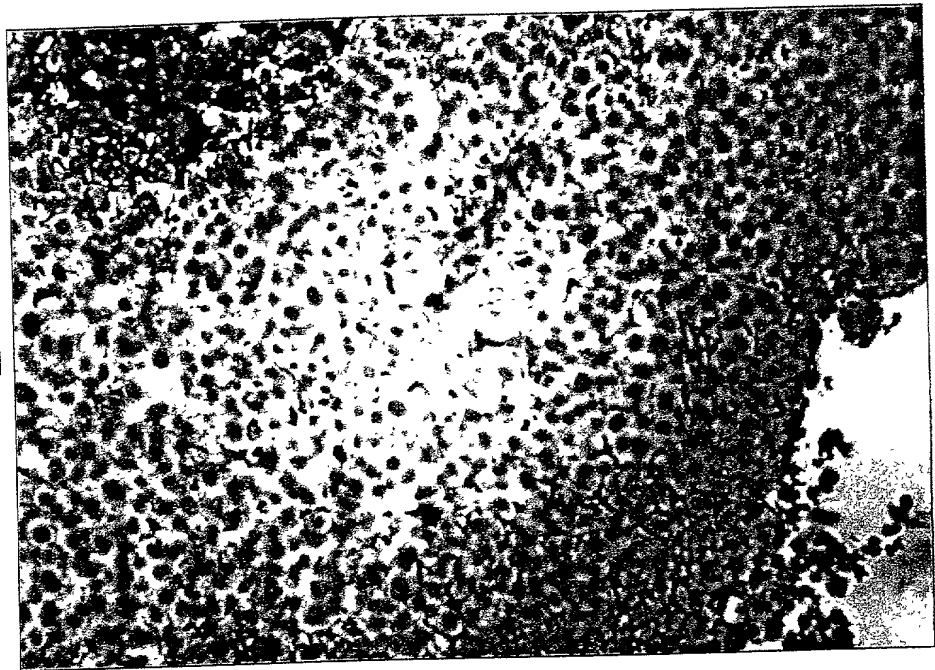
FIG. 70



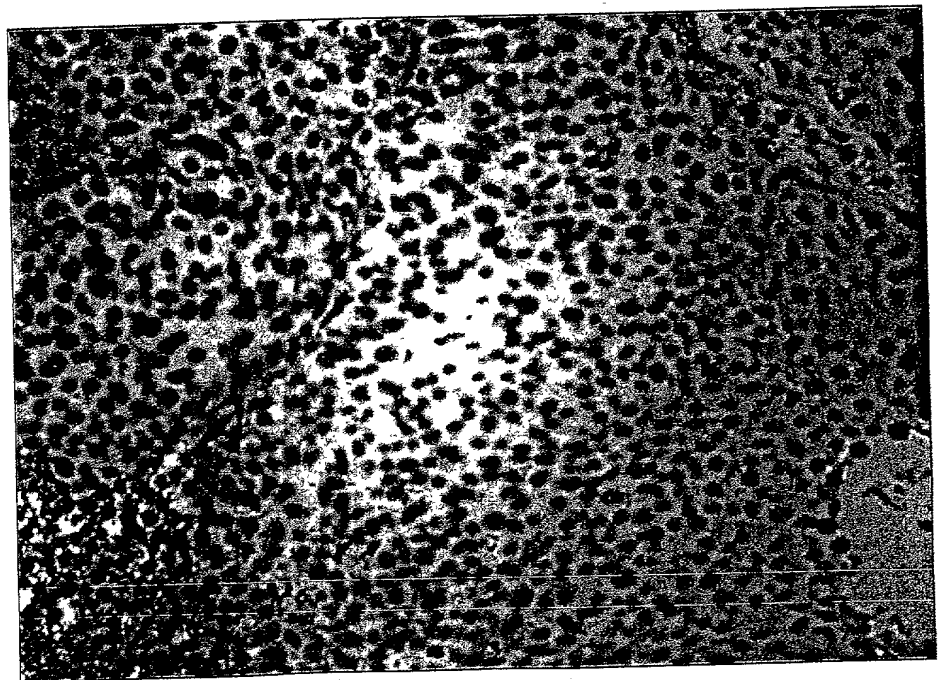
035431.072501

FIG. 71

3C5 Treated



mIgG Treated



09854811.072501

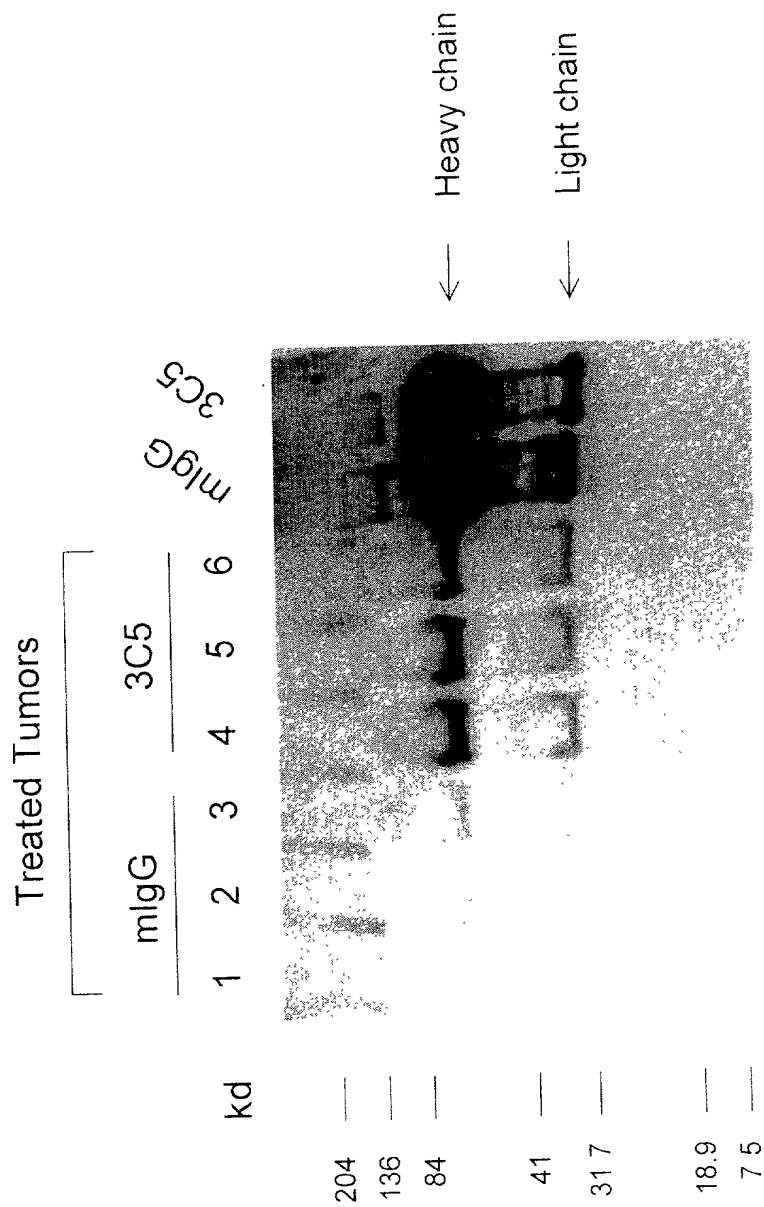


FIG. 72

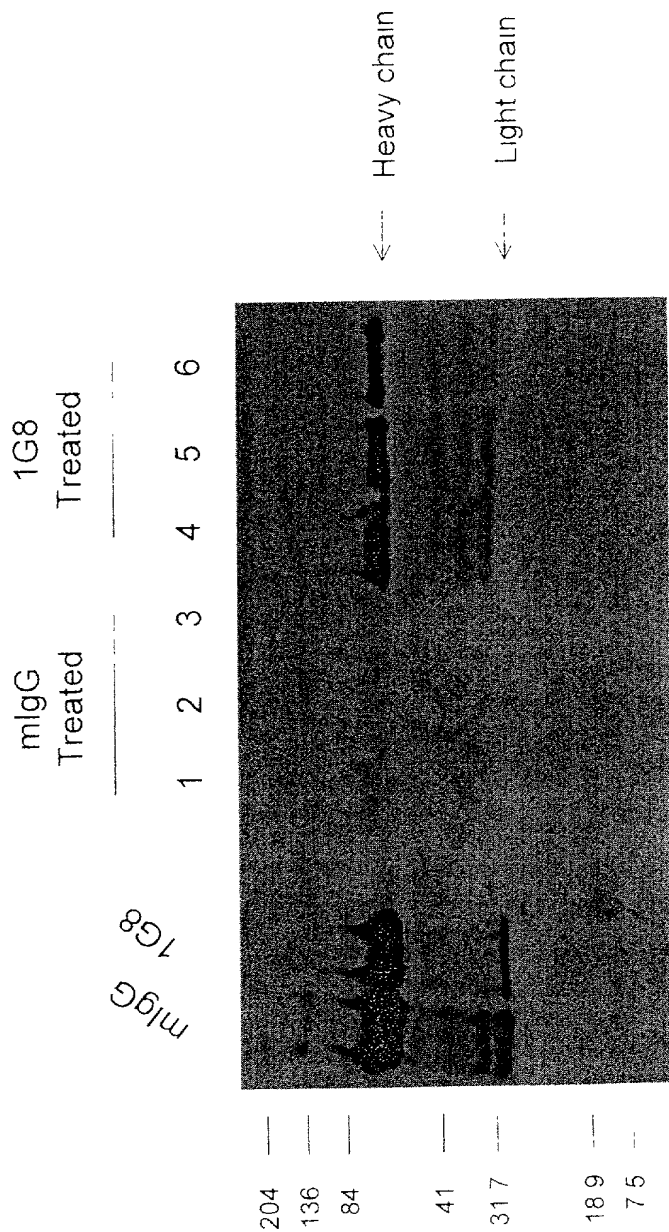


FIG. 73